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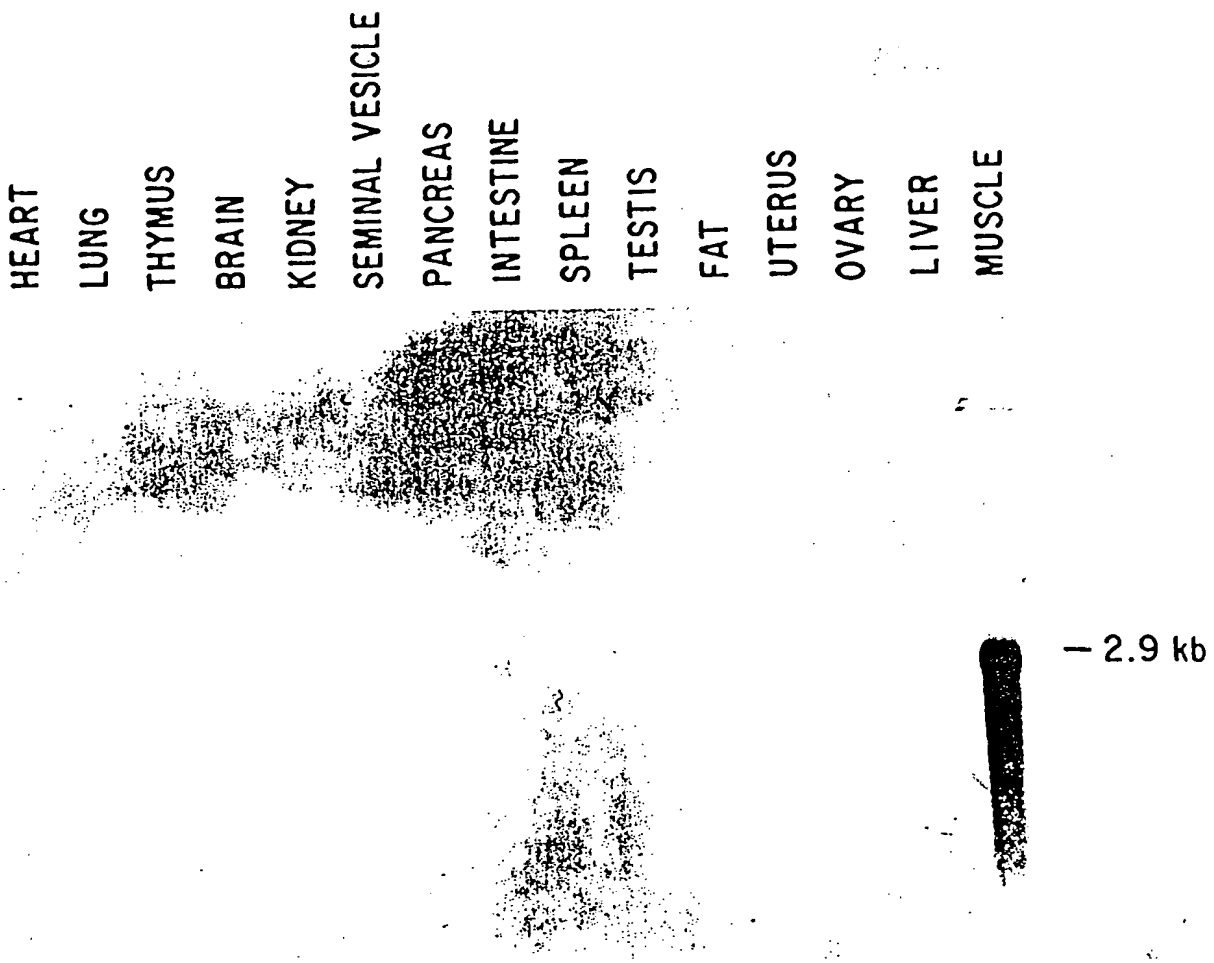
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THYMUS
BRAIN
KIDNEY
SEMINAL VESICLE
PANCREAS
INTESTINE
SPLEEN
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UTERUS
OVARY
LIVER
MUSCLE
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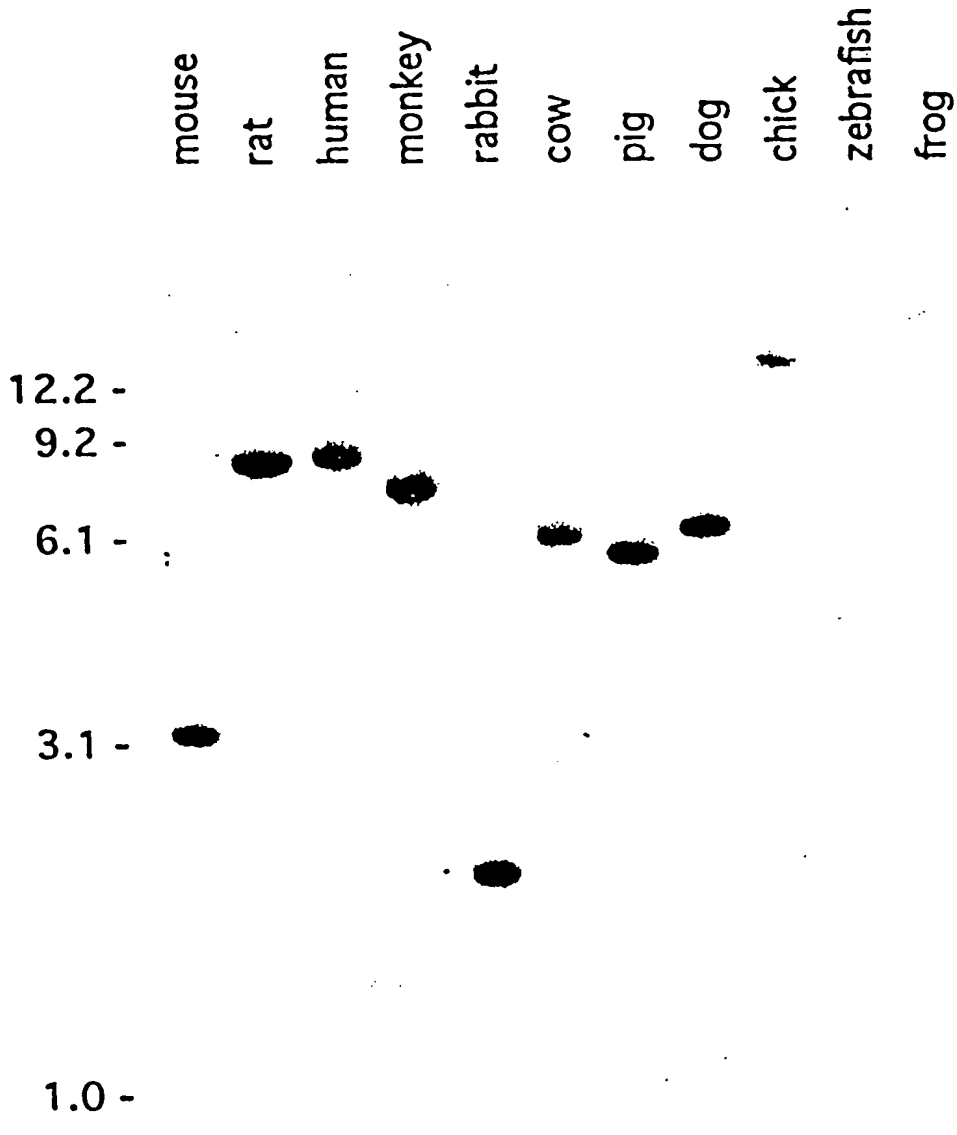
FIG. 1A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rat
human
monkey
rabbit
cow
pig
dog
chick
zebrafish
frog
12.2 -
9.2 -
6.1 -
3.1 -
1.0 -

FIG. 1B

```
1   TTAAGGTAGGAAGGATTTCAGGCTCTATTTACATAATTGTTCTTTCCTTTTCACACAGAA  60
                                                              N
61  TCCCTTTTTAGAAGTCAAGGTGACAGACACACCCAAGAGGTCCCGGAGAGACTTTGGGCT  120
      P  F  L  E  V  K  V  T  D  T  P [K  R] S [R  R] D  F  G  L
121 TGACTGCGATGAGCACTCCACGGAATCCCGGTGCTGCCGCTACCCCCTCACGGTCGATTT  180
      D  C  D  E  H  S  T  E  S  R  C  C  R  Y  P  L  T  V  D  F
181 TGAAGCCTTTGGATGGGACTGGATTATCGCACCCAAAAGATATAAGGCCAATTACTGCTC  240
      E  A  F  G  W  D  W  I  I  A  P  K  R  Y  K  A  N  Y  C  S
241 AGGAGAGTGTGAATTTGTGTTTTTACAAAAATATCCGCATACTCATCTTGTGCACCAAGC  300
      G  E  C  E  F  V  F  L  Q  K  Y  P  H  T  H  L  V  H  Q  A
301 AAACCCCAGAGGCTCAGCAGGCCCTTGCTGCACTCCGACAAAAATGTCTCCCATTAATAT  360
      N  P  R  G  S  A  G  P  C  C  T  P  T  K  M  S  P  I  N  M
361 GCTATATTTTAATGGCAAAGAACAAATAATATATGGGAAAATTCCAGCCATGGTAGTAGA  420
      L  Y  F  N  G  K  E  Q  I  I  Y  G  K  I  P  A  M  V  V  D
421 CCGCTGTGGGTGCTCATGAGCTTTGCATTAGGTTAGAAACTTCCCAAGTCATGGAAGGTC  480
      R  C  G  C  S  *
481 TTCCCCTCAATTTCGAAACTGTGAATTCCTGCAGCCCGGGGGATCCACTAGTTCTAGAGC  540
541 GGCCGCCACC  550
```

FIG. 2A

```
1   CAAAAAGATCCAGAAGGGATTTTGGTCTTGACTGTGATGAGCACTCAACAGAATCACGAT  60
    [K  R] S [R  R] D  F  G  L  D  C  D  E  H  S  T  E  S  R  C
61  GCTGTCGTTACCCTCTAACTGTGGATTTTGAAGCTTTTGGATGGGATTGGATTATCGCTC  120
      C  R  Y  P  L  T  V  D  F  E  A  F  G  W  D  W  I  I  A  P
121 CTAAAAGATATAAGGCCAATTACTGCTCTGGAGAGTGTGAATTTGTATTTTTACAAAAAT  180
      K  R  Y  K  A  N  Y  C  S  G  E  C  E  F  V  F  L  Q  K  Y
181 ATCCTCATACTCATCTGGTACACCAAGCAAACCCCAGAGGTTCAGCAGGCCCTTGCTGTA  240
      P  H  T  H  L  V  H  Q  A  N  P  R  G  S  A  G  P  C  C  T
241 CTCCCACAAAGATGTCTCCAATTAATATGCTATATTTTAATGGCAAAGAACAAATAATAT  300
      P  T  K  M  S  P  I  N  M  L  Y  F  N  G  K  E  Q  I  I  Y
301 ATGGGAAAATTCCAGCGATGGTAGTA  326
      G  K  I  P  A  M  V  V
```

FIG. 2B

```
GAA GAT GGG CTG AAT CCC TTT TTA GAA GTC AAA GTA ACA GAC ACA CCC AAG AGG TCC CGG
 E   D   G   L   N   P   F   L   E   V   K   V   T   D   T   P   K   R   S   R

AGA GAC TTT GGG CTT GAC TGT GAT GAA CAC TCC ACG GAA TCG CGG TGC TGT CGC TAC CCC
 R   D   F   G   L   D   C   D   E   H   S   T   E   S   R   C   C   R   Y   P

CTC ACG GTC GAT TTC GAA GCC TTT GGA TGG GAC TGG ATT ATT GCA CCC AAA AGA TAT AAG
 L   T   V   D   F   E   A   F   G   W   D   W   I   I   A   P   K   R   Y   K

GCT AAT TAC TGC TCT GGA GAG TGT GAA TTT GTG TTC TTA CAA AAA TAT CCG CAT ACT CAT
 A   N   Y   C   S   G   E   C   E   F   V   F   L   Q   K   Y   P   H   T   H

CTT GTG CAC CAA GCA AAC CCC AGA GGC TCG GCA GGC CCT TGC TGC ACG CCA ACA AAA ATG
 L   V   H   Q   A   N   P   R   G   S   A   G   P   C   C   T   P   T   K   M

TCT CCC ATT AAT ATG CTA TAT TTT AAT GGC AAA GAA CAA ATA ATA TAT GGG AAA ATT CCA
 S   P   I   N   M   L   Y   F   N   G   K   E   Q   I   I   Y   G   K   I   P

GCC ATG GTA GTA GAC CGG TGT GGG TGC TCG TGA GCT TTG CAT TAG CTT TAA AAT TTC CCA
 A   M   V   V   D   R   C   G   C   S

AAT CGT GGA AGG TCT TCC CCT CGA TTT CGA AAC TGT GAA TTT ATG TAC CAC AGG CTG TAG
```

RAT GDF-8

FIG. 2C

TTA GTA GTA AAG GCA CAA TTA TGG ATA TAC TTG AGG CAA GTC CAA AAA CCT ACA ACG GTG
L V V K A Q L W I Y L R Q V Q K P T T V

TTT GTG CAG ATC CTG AGA CTC ATT AAG CCC ATG AAA GAC GGT ACA AGA TAT ACT GGA ATT
F V Q I L R L I K P M K D G T R Y T G I

GGA TCT TTG AAA CTT GAC ATG AAC CCA GGC ACT GGT ATC TGG CAG AGT ATT GAT GTG AAG
G S L K L D M N P G T G I W Q S I D V K

ACA GTG CTG CAA AAT TGG CTC AAA ACG CCT GAA TCC AAT TTA GGC ATC GAA ATA AAA GCT
T V L Q N W L K Q P E S N L G I E I K A

TTT GAT GAG ACT GGA CGA GAT CTT GCT GTC ACA TTC CCA GGA CCG GGT GAA GAT GGA TTG
F D E T G R D L A V T F P G P G E D G L

AAC CCA TTT TTA GAG GTC AGA GTT ACA GAC ACA CCG AAA CGG TCC CGC AGA GAT TTT GGC
N P F L E V R V T D T P K R S R R D F G

CTT GAC TGT GAT GAG CAC TCA ACG GAA TCC CGA TGT TGT CGC TAC CCG CTG ACA GTG GAT
L D C D E H S T E S R C C R Y P L T V D

TTC GAA GCT TTT GGA TGG GAC TGG ATT ATA GCA CCT AAA AGA TAC AAA GCC AAT TAC TGC
F E A F G W D W I I A P K R Y K A N Y C

TCC GGA GAA TGC GAA TTT GTG TTT CTA CAG AAA TAC CCG CAC ACT CAC CTG GTA CAC CAA
S G E C E F V F L Q K Y P H T H L V H Q

GCA AAT CCC AGA GGC TCA GCA GGC CCT TGC TGC ACA CCC ACC AAG ATG TCC CCT ATA AAC
A N P R G S A G P C C T P T K M S P I N

ATG CTG TAT TTC AAT GGA AAA GAA CAA ATA ATA TAT GGA AAG ATA CCA GCC ATG GTT GTA
M L Y F N G K E Q I I Y G K I P A M V V

GAT CGT TGC GGG TGC TCA TGA GGC TGT CGT GAG ATC CAC CAT TCG ATA AAT TGT GGA AGC
D R C G C S

CAC CAA AAA AAA AAG CTA TAT CCC CTC ATC CAT CTT TGA AAC TGT GAA ATT ACG TAC GCT

AGG CAT TGC C

CHICKEN GDF-8

FIG. 2D

zebrafish.nucleotide
[Strand]

```
1     ATGCATTTTA CACAGGTTTT AATTTCTCTA AGTGTATTAA TTGCATGTGG TCCAGTGGGT TATGGAGATA
        M  H  F  T  Q  V  L  I  S  L  S  V  L  I  A  C  G  P  V  G  Y  G  D
71    TAACGGCGCA CCAGCAGCCT TCCACAGCCA CGGAGGAAAG CGAGCTGTGT TCCACATGTG AGTTCAGACA
        I  T  A  H  Q  Q  P  S  T  A  T  E  E  S  E  L  C  S  T  C  E  F  R  Q
141   ACACAGCAAG CTGATGAGAC TGCATGCCAT CAAGTCCCAA ATTCTTAGCA AACTCCGACT CAAGCAGGCT
        H  S  K  L  M  R  L  H  A  I  K  S  Q  I  L  S  K  L  R  L  K  Q  A
211   CCAAACATCA GCCGGGACGT GGTCAAGCAG CTGTTACCCA AAGCACCGCC TTTGCAACAA CTTCTGGATC
        P  N  I  S  R  D  V  V  K  Q  L  L  P  K  A  P  P  L  Q  Q  L  L  D
281   AGTACGATGT TTTAGGAGAT GACAGTAAGG ATGGAGCTGT GGAAGAGGAC GATGAACATG CCACCACAGA
        Q  Y  D  V  L  G  D  D  S  K  D  G  A  V  E  E  D  D  E  H  A  T  T  E
351   GACCATCATG ACCATGGCCA CAGAACCTGA CCCCATTGTT CAAGTAGATC GGAAACCGAA GTGTTGCTTT
        T  I  M  T  M  A  T  E  P  D  P  I  V  Q  V  D  R  K  P  K  C  C  F
421   TTCTCCTTCA GTCCGAAGAT CCAAGCGAAC CGGATCGTAA GAGCGCAGCT CTGGGTTCAT CTGAGACCGG
        F  S  F  S  P  K  I  Q  A  N  R  I  V  R  A  Q  L  W  V  H  L  R  P
491   CGGAGGAGGC GACCACCGTC TTCTTACAGA TATCTCGGCT GATGCCCGTT AAGGACGGAG GAAGACACCG
        A  E  E  A  T  T  V  F  L  Q  I  S  R  L  M  P  V  K  D  G  G  R  H  R
561   AATACGATCC CTGAAAATCG ACGTGAACGC AGGAGTCACG TCTTGGCAGA GTATAGACGT AAAGCAGGTG
        I  R  S  L  K  I  D  V  N  A  G  V  T  S  W  Q  S  I  D  V  K  Q  V
631   CTCACGGTGT GGTTAAAACA ACCGGAGACC AACCGAGGCA TCGAGATTAA CGCATATGAC GCGAAGGGAA
        L  T  V  W  L  K  Q  P  E  T  N  R  G  I  E  I  N  A  Y  D  A  K  G
701   ACGACTTGGC CGTCACTTCA ACCGAGACTG GGGAGGATGG ACTGCTCCCC TTTATGGAGG TGAAAATATC
        N  D  L  A  V  T  S  T  E  T  G  E  D  G  L  L  P  F  M  E  V  K  I  S
771   AGAGGGCCCA AAACGAATCC GGAGGGACTC CGGACTGGAC TGCGATGAGA ATTCCTCAGA GTCTCGCTGC
        E  G  P  K  R  I  R  R  D  S  G  L  D  C  D  E  N  S  S  E  S  R  C
841   TGCAGGTACC CTCTCACTGT GGACTTCGAG GACTTTGGCT GGGACTGGAT TATTGCTCCA AAACGCTATA
        C  R  Y  P  L  T  V  D  F  E  D  F  G  W  D  W  I  I  A  P  K  R  Y
911   AGGCGAATTA CTGTTCAGGA GAATGCGACT ACATGTACCT GCAGAAGTAT CCCCACACCC ATCTGGTGAA
        K  A  N  Y  C  S  G  E  C  D  Y  M  Y  L  Q  K  Y  P  H  T  H  L  V  N
981   CAAGGCCAGT CCGAGAGGAA CGGCTGGGCC CTGCTGCACT CCCACCAAGA TGTCTCCCAT CAACATGCTT
        K  A  S  P  R  G  T  A  G  P  C  C  T  P  T  K  M  S  P  I  N  M  L
1051  TACTTTAACG GCAAAGAGCA GATCATCTAC GGCAAGATCC CTTCGATGGT AGTAGACCGC TGTGGCTGCT
        Y  F  N  G  K  E  Q  I  I  Y  G  K  I  P  S  M  V  V  D  R  C  G  C
1121  CATGA
        S  .
```

FIG. 2E

salmon GDF-8.nucleotide1
[Strand]

```
1    GGCAGCCGGA GACGAATTGG GGGATCGAGA TTAATGCGTT CGACTCGAAG GGAAATGATC TGGCCGTTAC
       Q  P  E  T  N  W  G  I  E  I  N  A  F  D  S  K  G  N  D  L  A  V  T
71   CTCAGCAGAA GCGGGAGAAG GACTGCAACC CTTCATGGAG GTGACGATTT CAGAGGGCCC GAAGCGCTCC
       S  A  E  A  G  E  G  L  Q  P  F  M  E  V  T  I  S  E  G  P  K  R  S
141  AGGAGAGACT CGGGCCTGGA CTGTGACGAG AACTCCCCCG AGTCCCGCTG TTGCCGCTAC CCCCTCACGG
       R  R  D  S  G  L  D  C  D  E  N  S  P  E  S  R  C  C  R  Y  P  L  T
211  TAGACTTTGA AGACTTTGGC TGGGACTGGA TTATTGCCCC CAAGCGCTAC AAGGCCAACT ACTGCTCTGG
       V  D  F  E  D  F  G  W  D  W  I  I  A  P  K  R  Y  K  A  N  Y  C  S  G
281  TGAGTGTGAG TACATGCACC TGCAGAAGTA CCCCCACACC CACCTGGTGA ACAAGGCTAA CCCTCGCGGC
       E  C  E  Y  M  H  L  Q  K  Y  P  H  T  H  L  V  N  K  A  N  P  R  G
351  ACCGCAGGGC CCTGCTGCAC CCCCACCAAG ATGTCCCCCA TCAACATGCT CTACTTCAAC CGCAAAGAGC
       T  A  G  P  C  C  T  P  T  K  M  S  P  I  N  M  L  Y  F  N  R  K  E
421  AGATCATCTA CGGCAAGATC CCCTCCATGG TGGTGGACCG TTGCGGATGC TCGTGA
       Q  I  I  Y  G  K  I  P  S  M  V  V  D  R  C  G  C  S  .
```

FIG. 2F

salmon GDF8.nucleotide2
[Strand]

```
1    GGTTACCTCA ACTGAAGCCG GAGAAGGACT GCAACCCTTC ATGGAGGTGA AGATTTCGGA GGGCCCGAAG
       V  T  S  T  E  A  G  E  G  L  Q  P  F  M  E  V  K  I  S  E  G  P  K
71   CGCTCCAGGA GAGATTCGGG CCTGGACTGT GATGAGAACT CCCCCGAGTC CCGCTGCTGC CGGTACCCCC
       R  S  R  R  D  S  G  L  D  C  D  E  N  S  P  E  S  R  C  C  R  Y  P
141  TCACGGTGGA CTTTGAAGAC TTTGGCTGGG ACTGGATTAT TGCCCCCAAG CGCTACAAGG CCAACTACTG
       L  T  V  D  F  E  D  F  G  W  D  W  I  I  A  P  K  R  Y  K  A  N  Y  C
211  CTCTGGTGAG TGCGAGTACA TGCACCTGCA GAAGTACCCC CACACCCACC TGGTGAACAA GGCTAACCCT
         S  G  E  C  E  Y  M  H  L  Q  K  Y  P  H  T  H  L  V  N  K  A  N  P
281  CGCGGCACCG CGGGGCCCTG CTGCACCCCC ACCAAGATGT CCCCCATCAA CATGCTCTAC TTCAACCGCA
       R  G  T  A  G  P  C  C  T  P  T  K  M  S  P  I  N  M  L  Y  F  N  R
351  AAGAGCAGAT CATCTACGGC AAGATCCCCT CCATGGTGGT GGACCGCTGC GGCTGCTCGT GA
       K  E  Q  I  I  Y  G  K  I  P  S  M  V  V  D  R  C  G  C  S  .
```

FIG. 2G

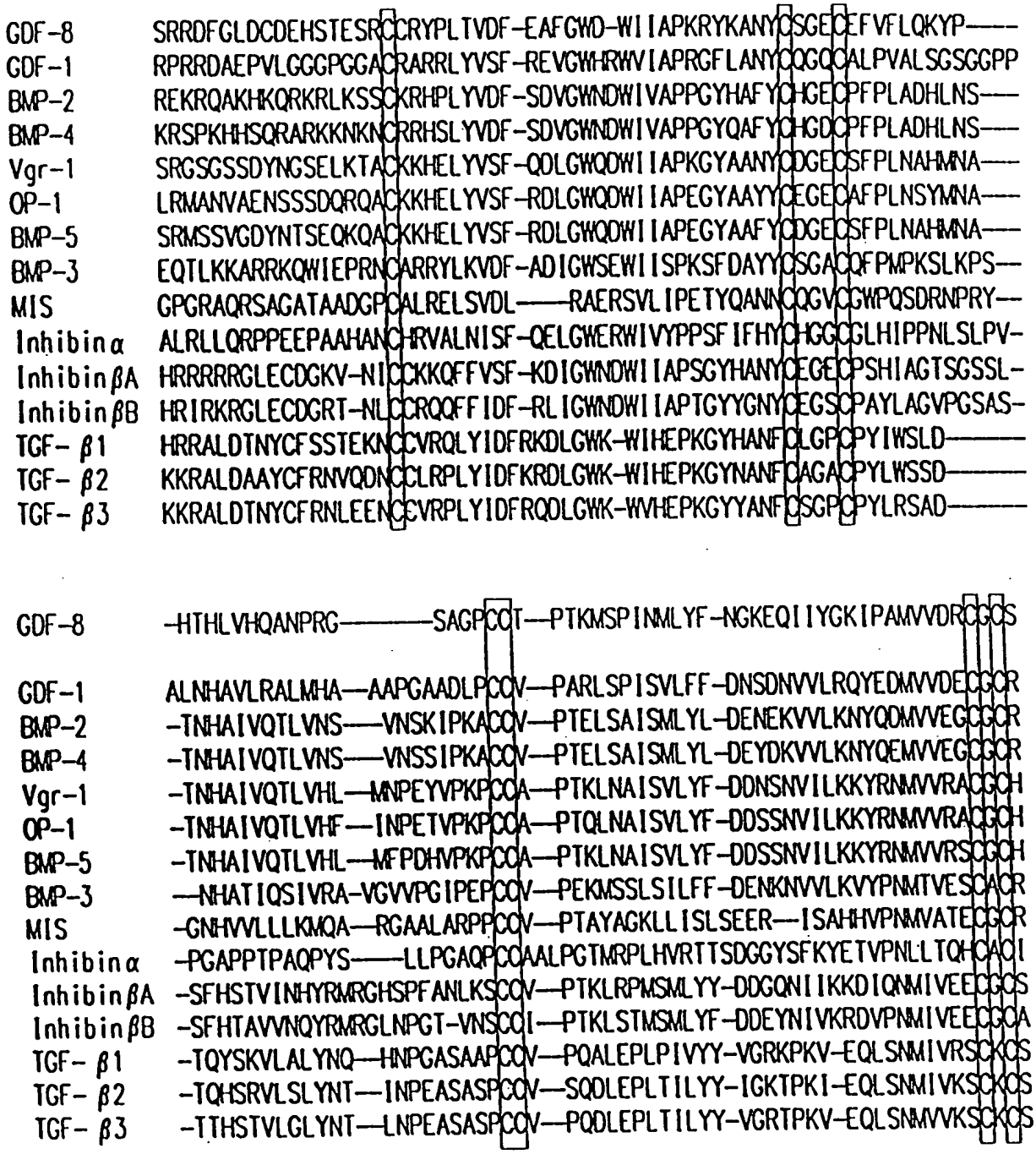
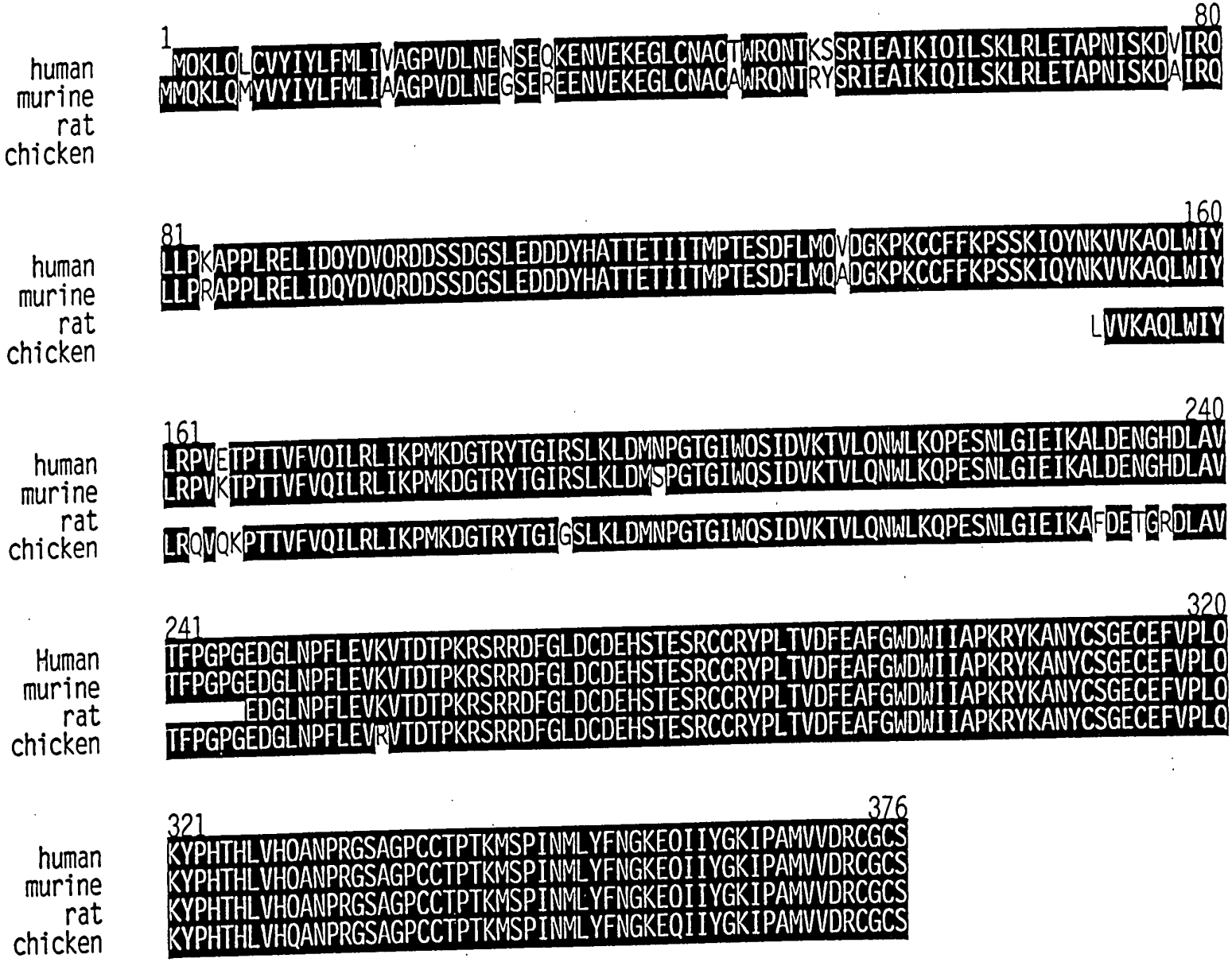

GDF-8 SRRDFGLDCDEHSTESRCCRYPLTVDF-EAFGWD-WIIAPKRYKANYCSGECEFVFLQKYP----
GDF-1 RPRRDAEPVLGGGPGGACRARRLYVSF-REVGWHRWVIAPRGFLANYCQGQCALPVALSGSGGPP
BMP-2 REKRQAKHKQRKRLKSSCKRHPLYVDF-SDVGWNDWIVAPPGYHAFYCHGECPFPLADHLNS----
BMP-4 KRSPKHHSQRARKKNKNCRRHSLYVDF-SDVGWNDWIVAPPGYQAFYCHGDCPFPLADHLNS----
Vgr-1 SRGSGSSDYNGSELKTACKKHELYVSF-QDLGWQDWIIAPKGYAANYCDGECSFPLNAHMNA----
OP-1 LRMANVAENSSSDQRQACKKHELYVSF-RDLGWQDWIIAPEGYAAYYCEGECAFPLNSYMNA----
BMP-5 SRMSSVGDYNTSEQKQACKKHELYVSF-RDLGWQDWIIAPEGYAAFYCDGECSFPLNAHMNA----
BMP-3 EQTLKKARRKQWIEPRNCARRYLKVDF-ADIGWSEWIISPKSFDAYYCSGACQFPMPKSLKPS---
MIS GPGRAQRSAGATAADGPCALRELSVDL----RAERSVLIPETYQANNCQGVCGWPQSDRNPRY---
Inhibin α ALRLLQRPPEEPAAHANCHRVALNISF-QELGWERWIVYPPSFIFHYCHGGCGLHIPPNLSLPV-
Inhibin βA HRRRRRGLECDGKV-NICCKKQFFVSF-KDIGWNDWIIAPSGYHANYCEGECPSHIAGTSGSSL-
Inhibin βB HRIRKRGLECDGRT-NLCCRQQFFIDF-RLIGWNDWIIAPTGYYGNYCEGSCPAYLAGVPGSAS-
TGF- β1 HRRALDTNYCFSSTEKNCCVRQLYIDFRKDLGWK-WIHEPKGYHANFCLGPCPYIWSLD------
TGF- β2 KKRALDAAYCFRNVQDNCCLRPLYIDFKRDLGWK-WIHEPKGYNANFCAGACPYLWSSD------
TGF- β3 KKRALDTNYCFRNLEENCCVRPLYIDFRQDLGWK-WVHEPKGYYANFCSGPCPYLRSAD------
GDF-8 -HTHLVHQANPRG-------SAGPCCT--PTKMSPINMLYF-NGKEQIIYGKIPAMVVDRCGCS
GDF-1 ALNHAVLRALMHA--AAPGAADLPCCV--PARLSPISVLFF-DNSDNVVLRQYEDMVVDECGCR
BMP-2 -TNHAIVQTLVNS--VNSKIPKACCV--PTELSAISMLYL-DENEKVVLKNYQDMVVEGCGCR
BMP-4 -TNHAIVQTLVNS--VNSSIPKACCV--PTELSAISMLYL-DEYDKVVLKNYQEMVVEGCGCR
Vgr-1 -TNHAIVQTLVHL--MNPEYVPKPCCA--PTKLNAISVLYF-DDNSNVILKKYRNMVVRACGCH
OP-1 -TNHAIVQTLVHF--INPETVPKPCCA--PTQLNAISVLYF-DDSSNVILKKYRNMVVRACGCH
BMP-5 -TNHAIVQTLVHL--MFPDHVPKPCCA--PTKLNAISVLYF-DDSSNVILKKYRNMVVRSCGCH
BMP-3 --NHATIQSIVRA-VGVVPGIPEPCCV--PEKMSSLSILFF-DENKNVVLKVYPNMTVESCACR
MIS -GNHVVLLLKMQA--RGAALARPPCCV--PTAYAGKLLISLSEER--ISAHHVPNMVATECGCR
Inhibin α -PGAPPTPAQPYS----LLPGAQPCCAALPGTMRPLHVRTTSDGGYSFKYETVPNLLTQHCACI
Inhibin βA -SFHSTVINHYRMRGHSPFANLKSCCV--PTKLRPMSMLYY-DDGQNIIKKDIQNMIVEECGCS
Inhibin βB -SFHTAVVNQYRMRGLNPGT-VNSCCI--PTKLSTMSMLYF-DDEYNIVKRDVPNMIVEECGCA
TGF- β1 -TQYSKVLALYNQ--HNPGASAAPCCV--PQALEPLPIVYY-VGRKPKV-EQLSNMIVRSCKCS
TGF- β2 -TQHSRVLSLYNT--INPEASASPCCV--SQDLEPLTILYY-IGKTPKI-EQLSNMIVKSCKCS
TGF- β3 -TTHSTVLGLYNT--LNPEASASPCCV--PQDLEPLTILYY-VGRTPKV-EQLSNMVVKSCKCS

FIG. 3A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murine
rat
chicken
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81
160
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LLPRAPPLRELIDQYDVQRDDSSDGSLEDDDYHATTETIITMPTESDFLMQADGKPKCCFFKPSSKIQYNKVVKAQLWIY
LVVKAQLWIY
161
240
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LRPVKTPTTVFVQILRLIKPMKDGTRYTGIRSLKLDMSPGTGIWQSIDVKTVLQNWLKQPESNLGIEIKALDENGHDLAV
LRQVQKPTTVFVQILRLIKPMKDGTRYTGIGSLKLDMNPGTGIWQSIDVKTVLQNWLKQPESNLGIEIKAFDETGRDLAV
241
320
Human
murine
rat
chicken
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TFPGPGEDGLNPFLEVRVTDTPKRSRRDFGLDCDEHSTESRCCRYPLTVDFEAFGWDWIIAPKRYKANYCSGECEFVPLQ
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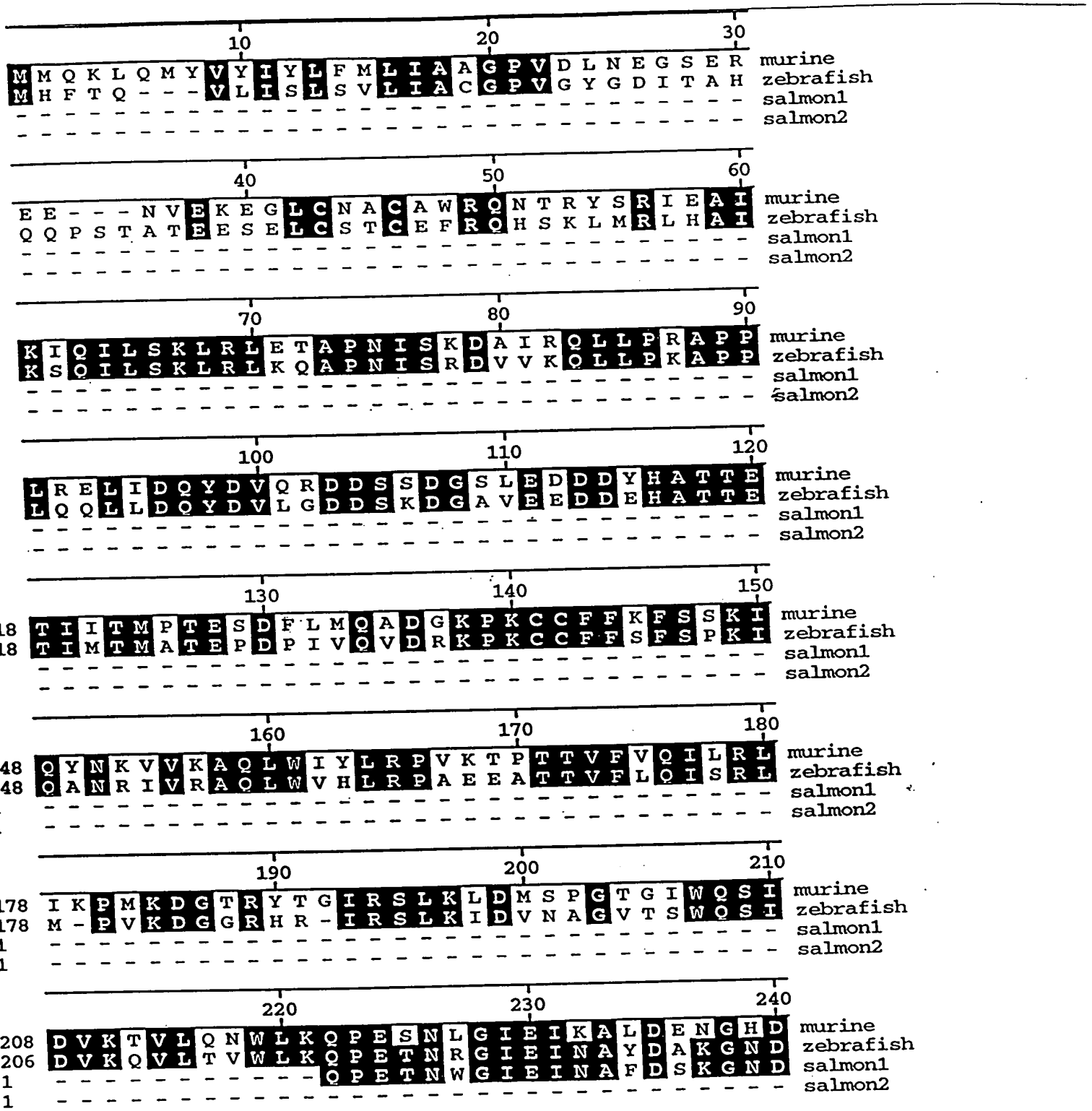
FIG. 3B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salmon1
salmon2
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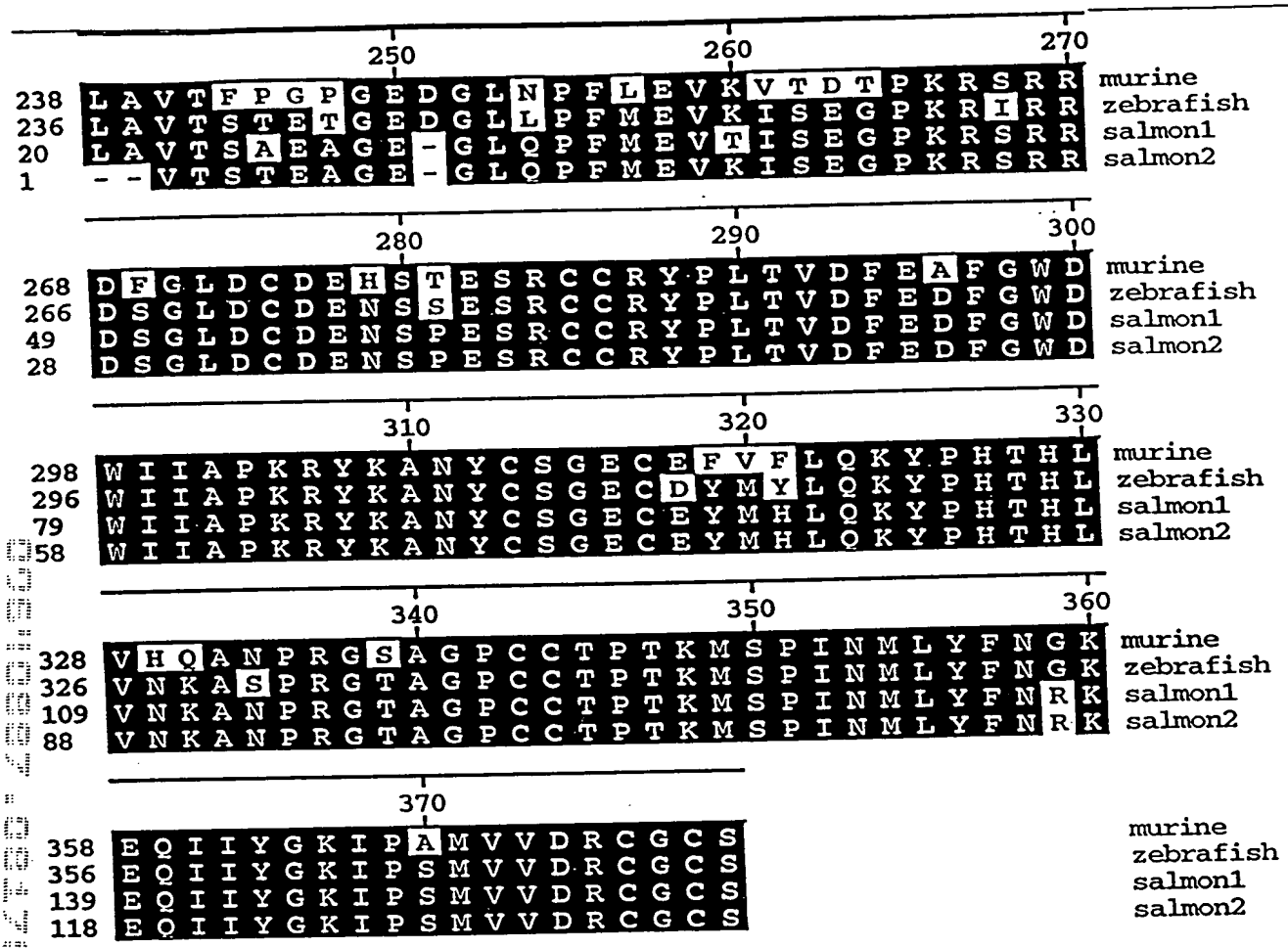
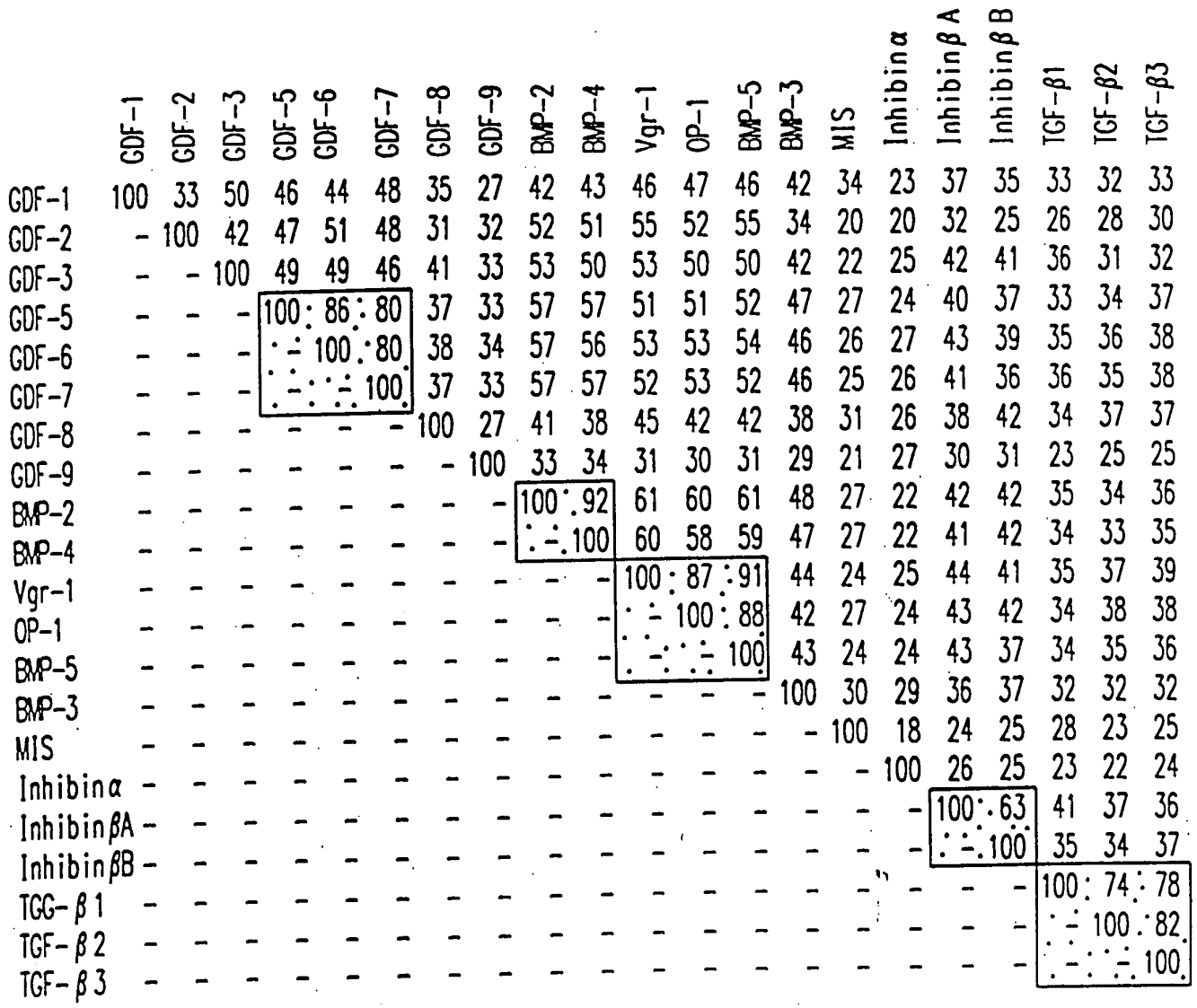
QQPSTATEESELCSTCEFRQHSKLMRLHAI zebrafish
salmon1
salmon2
70 80 90
KIQILSKLRLETAPNISKDAIRQLLPRAPP murine
KSQILSKLRLKQAPNISRDVVKQLLPKAPP zebrafish
salmon1
salmon2
100 110 120
LRELIDQYDVQRDDSSDGSLEDDDYHATTE murine
LQQLLDQYDVLGDDSKDGAVEEDDEHATTE zebrafish
salmon1
salmon2
130 140 150
TIITMPTESDFLMQADGKPKCCFFKFSSKI murine
TIMTMATEPDPIVQVDRKPKCCFFSFSPKI zebrafish
salmon1
salmon2
160 170 180
QYNKVVKAQLWIYLRPVKTPTTVFVQILRL murine
QANRIVRAQLWVHLRPAEEATTVFLQISRL zebrafish
salmon1
salmon2
190 200 210
IKPMKDGTRYTGIRSLKLDMSPGTGIWQSI murine
M-PVKDGGRHR-IRSLKIDVNAGVTSWQSI zebrafish
salmon1
salmon2
220 230 240
DVKTVLQNWLKQPESNLGIEIKALDENGHD murine
DVKQVLTVWLKQPETNRGIEINAYDAKGND zebrafish
QPETNWGIEINAFDSKGND salmon1
salmon2

FIG. 3C



Decoration 'Decoration #1': Shade (with solid black) residues that match the Consensus exactly.

FIG. 3D



	GDF-1	GDF-2	GDF-3	GDF-5	GDF-6	GDF-7	GDF-8	GDF-9	BMP-2	BMP-4	Vgr-1	OP-1	BMP-5	BMP-3	MIS	Inhibinα	InhibinβA	InhibinβB	TGF-β1	TGF-β2	TGF-β3
GDF-1	100	33	50	46	44	48	35	27	42	43	46	47	46	42	34	23	37	35	33	32	33
GDF-2	–	100	42	47	51	48	31	32	52	51	55	52	55	34	20	20	32	25	26	28	30
GDF-3	–	–	100	49	49	46	41	33	53	50	53	50	50	42	22	25	42	41	36	31	32
GDF-5	–	–	–	100	86	80	37	33	57	57	51	51	52	47	27	24	40	37	33	34	37
GDF-6	–	–	–	–	100	80	38	34	57	56	53	53	54	46	26	27	43	39	35	36	38
GDF-7	–	–	–	–	–	100	37	33	57	57	52	53	52	46	25	26	41	36	36	35	38
GDF-8	–	–	–	–	–	–	100	27	41	38	45	42	42	38	31	26	38	42	34	37	37
GDF-9	–	–	–	–	–	–	–	100	33	34	31	30	31	29	21	27	30	31	23	25	25
BMP-2	–	–	–	–	–	–	–	–	100	92	61	60	61	48	27	22	42	42	35	34	36
BMP-4	–	–	–	–	–	–	–	–	–	100	60	58	59	47	27	22	41	42	34	33	35
Vgr-1	–	–	–	–	–	–	–	–	–	–	100	87	91	44	24	25	44	41	35	37	39
OP-1	–	–	–	–	–	–	–	–	–	–	–	100	88	42	27	24	43	42	34	38	38
BMP-5	–	–	–	–	–	–	–	–	–	–	–	–	100	43	24	24	43	37	34	35	36
BMP-3	–	–	–	–	–	–	–	–	–	–	–	–	–	100	30	29	36	37	32	32	32
MIS	–	–	–	–	–	–	–	–	–	–	–	–	–	–	100	18	24	25	28	23	25
Inhibinα	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	100	26	25	23	22	24
InhibinβA	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	100	63	41	37	36
InhibinβB	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	100	35	34	37
TGG-β1	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	100	74	78
TGF-β2	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	100	82
TGF-β3	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	100

FIG. 4

```
1    GTCTCTCGGACGGTACATGCACTAATATTTCACTTGGCATTACTCAAAAGCAAAAAGAAG   60
61   AAATAAGAACAAGGGAAAAAAAAAAGATTGTGCTGATTTTTAAAATGATGCAAAAACTGCA  120
                                                  M  M  Q  K  L  Q
121  AATGTATGTTTATATTTACCTGTTCATGCTGATTGCTGCTGGCCCAGTGGATCTAAATGA   180
     M  Y  V  Y  I  Y  L  F  M  L  I  A  A  G  P  V  D  L  N  E
181  GGGCAGTGAGAGAGAAGAAAATGTGGAAAAAGAGGGGCTGTGTAATGCATGTGCGTGGAG  240
     G  S  E  R  E  E  N  V  E  K  E  G  L  C  N  A  C  A  W  R
241  ACAAAACACGAGGTACTCCAGAATAGAAGCCATAAAAATTCAAATCCTCAGTAAGCTGCG  300
     Q  N  T  R  Y  S  R  I  E  A  I  K  I  Q  I  L  S  K  L  R
301  CCTGGAAACAGCTCCTAACATCAGCAAAGATGCTATAAGACAACTTCTGCCAAGAGCGCC  360
     L  E  T  A  P  [N  I  S]  K  D  A  I  R  Q  L  L  P  R  A  P
361  TCCACTCCGGGAACTGATCGATCAGTACGACGTCCAGAGGGATGACAGCAGTGATGGCTC  420
     P  L  R  E  L  I  D  Q  Y  D  V  Q  R  D  D  S  S  D  G  S
421  TTTGGAAGATGACGATTATCACGCTACCACGGAAACAATCATTACCATGCCTACAGAGTC  480
     L  E  D  D  D  Y  H  A  T  T  E  T  I  I  T  M  P  T  E  S
481  TGACTTTCTAATGCAAGCGGATGGCAAGCCCAAATGTTGCTTTTTTAAATTTAGCTCTAA  540
     D  F  L  M  Q  A  D  G  K  P  K  C  C  F  F  K  F  S  S  K
541  AATACAGTACAACAAAGTAGTAAAAGCCCAACTGTGGATATATCTCAGACCCGTCAAGAC  600
     I  Q  Y  N  K  V  V  K  A  Q  L  W  I  Y  L  R  P  V  K  T
601  TCCTACAACAGTGTTTGTGCAAATCCTGAGACTCATCAAACCCATGAAAGACGGTACAAG  660
     P  T  T  V  F  V  Q  I  L  R  L  I  K  P  M  K  D  G  T  R
661  GTATACTGGAATCCGATCTCTGAAACTTGACATGAGCCCAGGCACTGGTATTTGGCAGAG  720
     Y  T  G  I  R  S  L  K  L  D  M  S  P  G  T  G  I  W  Q  S
721  TATTGATGTGAAGACAGTGTTGCAAAATTGGCTCAAACAGCCTGAATCCAACTTAGGCAT  780
     I  D  V  K  T  V  L  Q  N  W  L  K  Q  P  E  S  N  L  G  I
781  TGAAATCAAAGCTTTGGATGAGAATGGCCATGATCTTGCTGTAACCTTCCCAGGACCAGG  840
     E  I  K  A  L  D  E  N  G  H  D  L  A  V  T  F  P  G  P  G
841  AGAAGATGGGCTGAATCCCTTTTTAGAAGTCAAGGTGACAGACACACCCAAGAGGTCCCG  900
     E  D  G  L  N  P  F  L  E  V  K  V  T  D  T  P  K  [R  S  R
901  GAGAGACTTTGGGCTTGACTGCGATGAGCACTCCACGGAATCCCGGTGCTGCCGCTACCC  960
     R]  D  F  G  L  D  C  D  E  H  S  T  E  S  R  C  C  R  Y  P
961  CCTCACGGTCGATTTTGAAGCCTTTGGATGGGACTGGATTATCGCACCCAAAAGATATAA  1020
     L  T  V  D  F  E  A  F  G  W  D  W  I  I  A  P  K  R  Y  K
1021 GGCCAATTACTGCTCAGGAGAGTGTGAATTTGTGTTTTTACAAAAATATCCGCATACTCA  1080
     A  N  Y  C  S  G  E  C  E  F  V  F  L  Q  K  Y  P  H  T  H
1081 TCTTGTGCACCAAGCAAACCCCAGAGGCTCAGCAGGCCCTTGCTGCACTCCGACAAAAAT  1140
     L  V  H  Q  A  N  P  R  G  S  A  G  P  C  C  T  P  T  K  M
1141 GTCTCCCATTAATATGCTATATTTTAATGGCAAAGAACAAATAATATATGGGAAAATTCC  1200
     S  P  I  N  M  L  Y  F  N  G  K  E  Q  I  I  Y  G  K  I  P
1201 AGCCATGGTAGTAGACCGCTGTGGGTGCTCATGAGCTTTGCATTAGGTTAGAAACTTCCC  1260
     A  M  V  V  D  R  C  G  C  S  *
```

FIG. 5A

1261 AAGTCATGGAAGGTCTTCCCCTCAATTTCGAAACTGTGAATTCAAGCACCACAGGCTGTA 1320
1321 GGCCTTGAGTATGCTCTAGTAACGTAAGCACAAGCTACAGTGTATGAACTAAAAGAGAGA 1380
1381 ATAGATGCAATGGTTGGCATTCAACCACCAAAATAAACCATACTATAGGATGTTGTATGA 1440
1441 TTTCCAGAGTTTTTGAAATAGATGGAGATCAAATTACATTTATGTCCATATATGTATATT 1500
1501 ACAACTACAATCTAGGCAAGGAAGTGAGAGCACATCTTGTGGTCTGCTGAGTTAGGAGGG 1560
1561 TATGATTAAAAGGTAAAGTCTTATTTCCTAACAGTTTCACTTAATATTTACAGAAGAATC 1620
1621 TATATGTAGCCTTTGTAAAGTGTAGGATTGTTATCATTTAAAAACATCATGTACACTTAT 1680
1681 ATTTGTATTGTATACTTGGTAAGATAAAATTCCACAAAGTAGGAATGGGGCCTCACATAC 1740
1741 ACATTGCCATTCCTATTATAATTGGACAATCCACCACGGTGCTAATGCAGTGCTGAATGG 1800
1801 CTCCTACTGGACCTCTCGATAGAACACTCTACAAAGTACGAGTCTCTCTCTCCCTTCCAG 1860
1861 GTGCATCTCCACACACACAGCACTAAGTGTTCAATGCATTTTCTTTAAGGAAAGAAGAAT 1920
1921 CTTTTTTTCTAGAGGTCAACTTTCAGTCAACTCTAGCACAGCGGGAGTGACTGCTGCATC 1980
1981 TTAAAAGGCAGCCAAACAGTATTCATTTTTTAATCTAAATTTCAAAATCACTGTCTGCCT 2040
2041 TTATCACATGGCAATTTTGTGGTAAAATAATGGAAATGACTGGTTCTATCAATATTGTAT 2100
2101 AAAAGACTCTGAAACAATTACATTTATATAATATGTATACAATATTGTTTTGTAAATAAG 2160
2161 TGTCTCCTTTTATATTTACTTTGGTATATTTTTACACTAATGAAATTTCAAATCATTAAA 2220
2221 GTACAAAGACATGTCATGTATCACAAAAAAGGTGACTGCTTCTATTTCAGAGTGAATTAG 2280
2281 CAGATTCAATAGTGGTCTTAAAACTCTGTATGTTAAGATTAGAAGGTTATATTACAATCA 2340
2341 ATTTATGTATTTTTTACATTATCAACTTATGGTTTCATGGTGGCTGTATCTATGAATGTG 2400
2401 GCTCCCAGTCAAATTTCAATGCCCCACCATTTTAAAAATTACAAGCATTACTAAACATAC 2460
2461 CAACATGTATCTAAAGAAATACAAATATGGTATCTCAATAACAGCTACTTTTTTATTTTA 2520
2521 TAATTTGACAATGAATACATTTCTTTTATTTACTTCAGTTTTATAAATTGGAACTTTGTT 2580
2581 TATCAAATGTATTGTACTCATAGCTAAATGAAATTATTTCTTACATAAAAATGTGTAGAA 2640
2641 ACTATAAATTAAAGTGTTTTCACATTTTTGAAAGGC 2676

FIG. 5B

```
1    AAGAAAAGTAAAAGGAAGAAACAAGAACAAGAAAAAAGATTATATTGATTTTAAAATCAT   60
                                                              M
61   GCAAAAACTGCAACTCTGTGTTTATATTTACCTGTTTATGCTGATTGTTGCTGGTCCAGT  120
       Q  K  L  Q  L  C  V  Y  I  Y  L  F  M  L  I  V  A  G  P  V
121  GGATCTAAATGAGAACAGTGAGCAAAAAGAAAATGTGGAAAAAGAGGGGCTGTGTAATGC  180
       D  L  N  E  N  S  E  Q  K  E  N  V  E  K  E  G  L  C  N  A
181  ATGTACTTGGAGACAAAACACTAAATCTTCAAGAATAGAAGCCATTAAGATACAAATCCT  240
       C  T  W  R  Q  N  T  K  S  S  R  I  E  A  I  K  I  Q  I  L
241  CAGTAAACTTCGTCTGGAAACAGCTCCTAACATCAGCAAAGATGTTATAAGACAACTTTT  300
       S  K  L  R  L  E  T  A  P  [N  I  S]  K  D  V  I  R  Q  L  L
301  ACCCAAAGCTCCTCCACTCCGGGAACTGATTGATCAGTATGATGTCCAGAGGGATGACAG  360
       P  K  A  P  P  L  R  E  L  I  D  Q  Y  D  V  Q  R  D  D  S
361  CAGCGATGGCTCTTTGGAAGATGACGATTATCACGCTACAACGGAAACAATCATTACCAT  420
       S  D  G  S  L  E  D  D  D  Y  H  A  T  T  E  T  I  I  T  M
421  GCCTACAGAGTCTGATTTTCTAATGCAAGTGGATGGAAAACCCAAATGTTGCTTCTTTAA  480
       P  T  E  S  D  F  L  M  Q  V  D  G  K  P  K  C  C  F  F  K
481  ATTTAGCTCTAAAATACAATACAATAAAGTAGTAAAGGCCCAACTATGGATATATTTGAG  540
       F  S  S  K  I  Q  Y  N  K  V  V  K  A  Q  L  W  I  Y  L  R
541  ACCCGTCGAGACTCCTACAACAGTGTTTGTGCAAATCCTGAGACTCATCAAACCTATGAA  600
       P  V  E  T  P  T  T  V  F  V  Q  I  L  R  L  I  K  P  M  K
601  AGACGGTACAAGGTATACTGGAATCCGATCTCTGAAACTTGACATGAACCCAGGCACTGG  660
       D  G  T  R  Y  T  G  I  R  S  L  K  L  D  M  N  P  G  T  G
661  TATTTGGCAGAGCATTGATGTGAAGACAGTGTTGCAAAATTGGCTCAAACAACCTGAATC  720
       I  W  Q  S  I  D  V  K  T  V  L  Q  N  W  L  K  Q  P  E  S
721  CAACTTAGGCATTGAAATAAAAGCTTTAGATGAGAATGGTCATGATCTTGCTGTAACCTT  780
       N  L  G  I  E  I  K  A  L  D  E  N  G  H  D  L  A  V  T  F
781  CCCAGGACCAGGAGAAGATGGGCTGAATCCGTTTTTAGAGGTCAAGGTAACAGACACACC  840
       P  G  P  G  E  D  G  L  N  P  F  L  E  V  K  V  T  D  T  P
841  AAAAAGATCCAGAAGGGATTTTGGTCTTGACTGTGATGAGCACTCAACAGAATCACGATG  900
       K  [R  S  R  R]  D  F  G  L  D  C  D  E  H  S  T  E  S  R  C
901  CTGTCGTTACCCTCTAACTGTGGATTTTGAAGCTTTTGGATGGGATTGGATTATCGCTCC  960
       C  R  Y  P  L  T  V  D  F  E  A  F  G  W  D  W  I  I  A  P
961  TAAAAGATATAAGGCCAATTACTGCTCTGGAGAGTGTGAATTTGTATTTTTACAAAAATA 1020
       K  R  Y  K  A  N  Y  C  S  G  E  C  E  F  V  F  L  Q  K  Y
1021 TCCTCATACTCATCTGGTACACCAAGCAAACCCCAGAGGTTCAGCAGGCCCTTGCTGTAC 1080
       P  H  T  H  L  V  H  Q  A  N  P  R  G  S  A  G  P  C  C  T
1081 TCCCACAAAGATGTCTCCAATTAATATGCTATATTTTAATGGCAAAGAACAAATAATATA 1140
       P  T  K  M  S  P  I  N  M  L  Y  F  N  G  K  E  Q  I  I  Y
1141 TGGGAAAATTCCAGCGATGGTAGTAGACCGCTGTGGGTGCTCATGAGATTTATATTAAGC 1200
       G  K  I  P  A  M  V  V  D  R  C  G  C  S  *
```

FIG. 5C

```
1201  GTTCATAACTTCCTAAAACATGGAAGGTTTTCCCCTCAACAATTTTGAAGCTGTGAAATT  1260
1261  AAGTACCACAGGCTATAGGCCTAGAGTATGCTACAGTCACTTAAGCATAAGCTACAGTAT  1320
1321  GTAAACTAAAAGGGGGAATATATGCAATGGTTGGCATTTAACCATCCAAACAAATCATAC  1380
1381  AAGAAAGTTTTATGATTTCCAGAGTTTTTGAGCTAGAAGGAGATCAAATTACATTTATGT  1440
1441  TCCTATATATTACAACATCGGCGAGGAAATGAAAGCGATTCTCCTTGAGTTCTGATGAAT  1500
1501  TAAAGGAGTATGCTTTAAAGTCTATTTCTTTAAAGTTTTGTTTAATATTTACAGAAAAAT  1560
1561  CCACATACAGTATTGGTAAAATGCAGGATTGTTATATACCATCATTCGAATCATCCTTAA  1620
1621  ACACTTGAATTTATATTGTATGGTAGTATACTTGGTAAGATAAAATTCCACAAAAATAGG  1680
1681  GATGGTGCAGCATATGCAATTTCCATTCCTATTATAATTGACACAGTACATTAACAATCC  1740
1741  ATGCCAACGGTGCTAATACGATAGGCTGAATGTCTGAGGCTACCAGGTTTATCACATAAA  1800
1801  AAACATTCAGTAAAATAGTAAGTTTCTCTTTTCTTCAGGTGCATTTTCCTACACCTCCAA  1860
1861  ATGAGGAATGGATTTTCTTTAATGTAAGAAGAATCATTTTTCTAGAGGTTGGCTTTCAAT  1920
1921  TCTGTAGCATACTTGGAGAAACTGCATTATCTTAAAAGGCAGTCAAATGGTGTTTGTTTT  1980
1981  TATCAAAATGTCAAAATAACATACTTGGAGAAGTATGTAATTTTGTCTTTGGAAAATTAC  2040
2041  AACACTGCCTTTGCAACACTGCAGTTTTTATGGTAAAATAATAGAAATGATCGACTCTAT  2100
2101  CAATATTGTATAAAAAAGACTGAAACAATGCATTTATATAATATGTATACAATATTGTTTT  2160
2161  GTAAATAAGTGTCTCCTTTTTTATTTACTTTGGTATATTTTTACACTAAGGACATTTCAA  2220
2221  ATTAAGTACTAAGGCACAAAGACATGTCATGCATCACAGAAAAGCAACTACTTATATTTC  2280
2281  AGAGCAAATTAGCAGATTAAATAGTGGTCTTAAAACTCCATATGTTAATGATTAGATGGT  2340
2341  TATATTACAATCATTTTATATTTTTTTACATGATTAACATTCACTTATGGATTCATGATG  2400
2401  GCTGTATAAAGTGAATTTGAAATTTCAATGGTTTACTGTCATTGTGTTTAAATCTCAACG  2460
2461  TTCCATTATTTTAATACTTGCAAAAACATTACTAAGTATACCAAAATAATTGACTCTATT  2520
2521  ATCTGAAATGAAGAATAAACTGATGCTATCTCAACAATAACTGTTACTTTTATTTTATAA  2580
2581  TTTGATAATGAATATATTTCTGCATTTATTTACTTCTGTTTTGTAAATTGGGATTTTGTT  2640
2641  AATCAAATTTATTGTACTATGACTAAATGAAATTATTTCTTACATCTAATTTGTAGAAAC  2700
2701  AGTATAAGTTATATTAAAGTGTTTTCACATTTTTTTGAAAGAC  2743
```

FIG. 5D

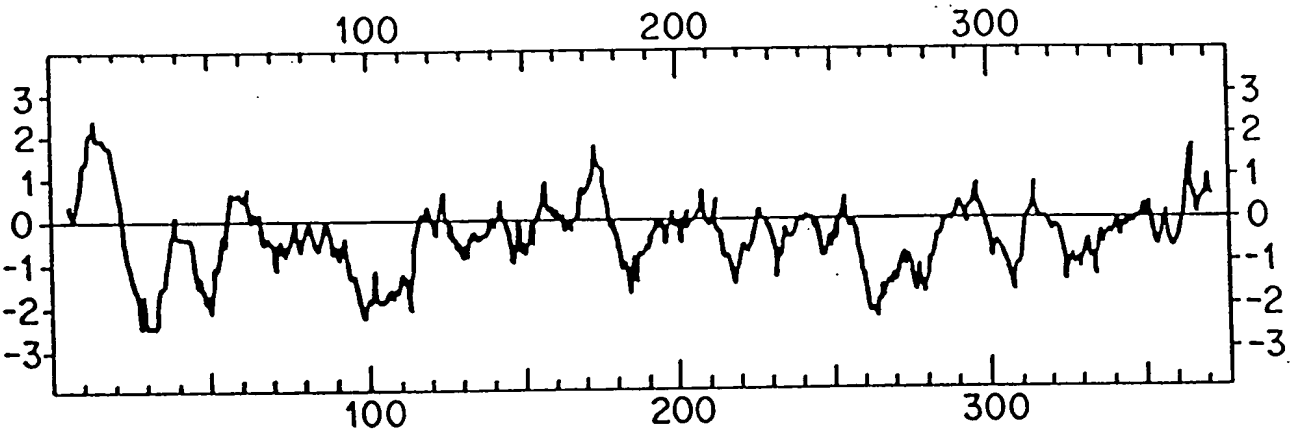


FIG. 6A

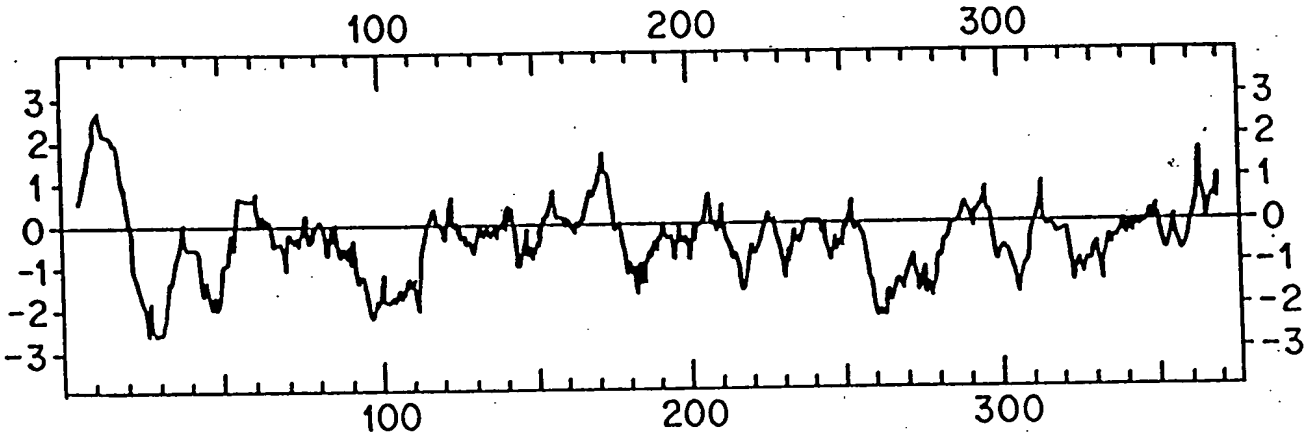


FIG. 6B

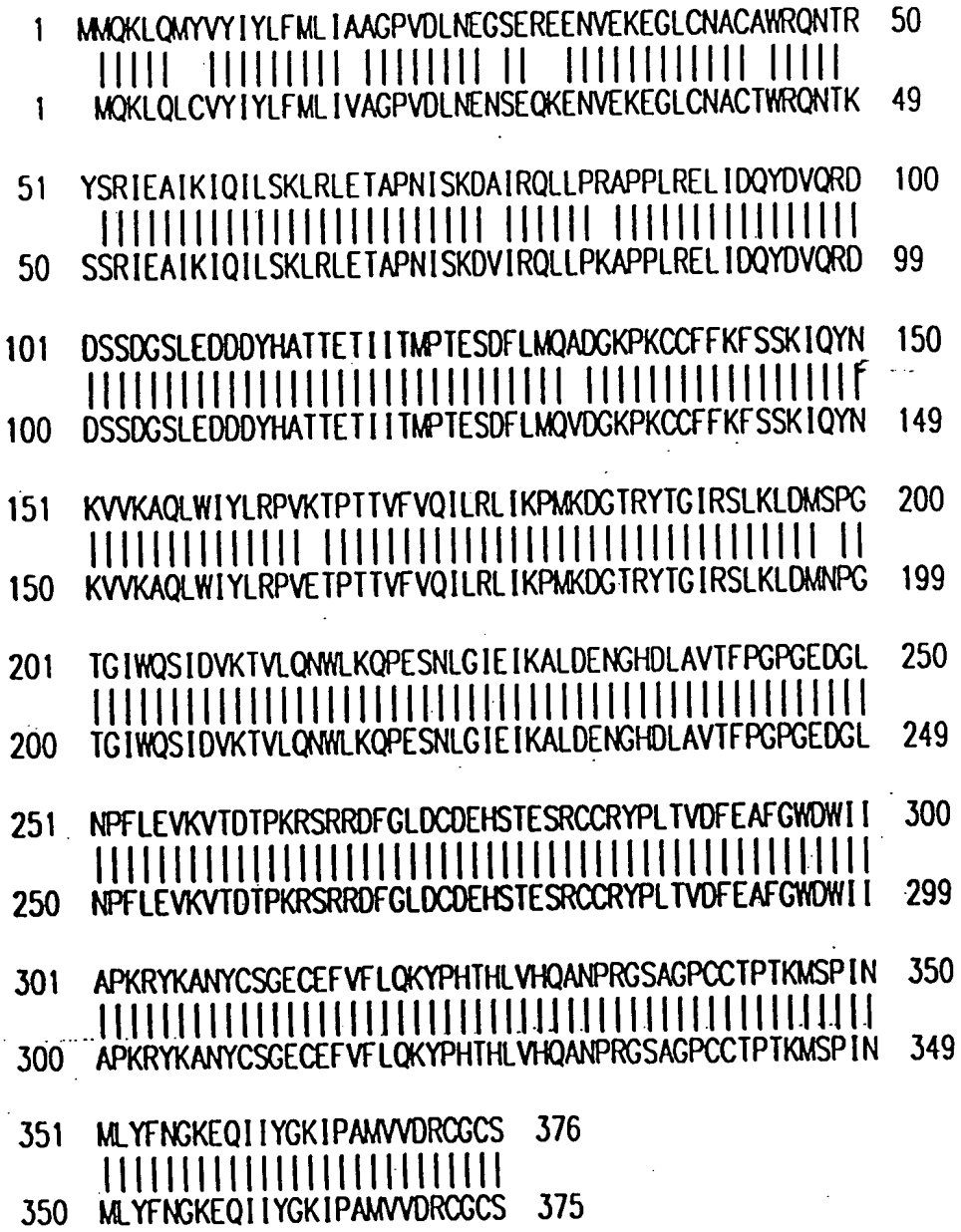

1 MMQKLQMYVYIYLFMLIAAGPVDLNEGSEREENVEKEGLCNACAWRQNTR 50
1 MQKLQLCVYIYLFMLIVAGPVDLNENSEQKENVEKEGLCNACTWRQNTK 49
51 YSRIEAIKIQILSKLRLETAPNISKDAIRQLLPRAPPLRELIDQYDVQRD 100
50 SSRIEAIKIQILSKLRLETAPNISKDVIRQLLPKAPPLRELIDQYDVQRD 99
101 DSSDGSLEDDDYHATTETIITMPTESDFLMQADGKPKCCFFKFSSKIQYN 150
100 DSSDGSLEDDDYHATTETIITMPTESDFLMQVDGKPKCCFFKFSSKIQYN 149
151 KVVKAQLWIYLRPVKTPTTVFVQILRLIKPMKDGTRYTGIRSLKLDMSPG 200
150 KVVKAQLWIYLRPVETPTTVFVQILRLIKPMKDGTRYTGIRSLKLDMNPG 199
201 TGIWQSIDVKTVLQNWLKQPESNLGIEIKALDENGHDLAVTFPGPGEDGL 250
200 TGIWQSIDVKTVLQNWLKQPESNLGIEIKALDENGHDLAVTFPGPGEDGL 249
251 NPFLEVKVTDTPKRSRRDFGLDCDEHSTESRCCRYPLTVDFEAFGWDWII 300
250 NPFLEVKVTDTPKRSRRDFGLDCDEHSTESRCCRYPLTVDFEAFGWDWII 299
301 APKRYKANYCSGECEFVFLQKYPHTHLVHQANPRGSAGPCCTPTKMSPIN 350
300 APKRYKANYCSGECEFVFLQKYPHTHLVHQANPRGSAGPCCTPTKMSPIN 349
351 MLYFNGKEQIIYGKIPAMVVDRCGCS 376
350 MLYFNGKEQIIYGKIPAMVVDRCGCS 375

FIG. 7

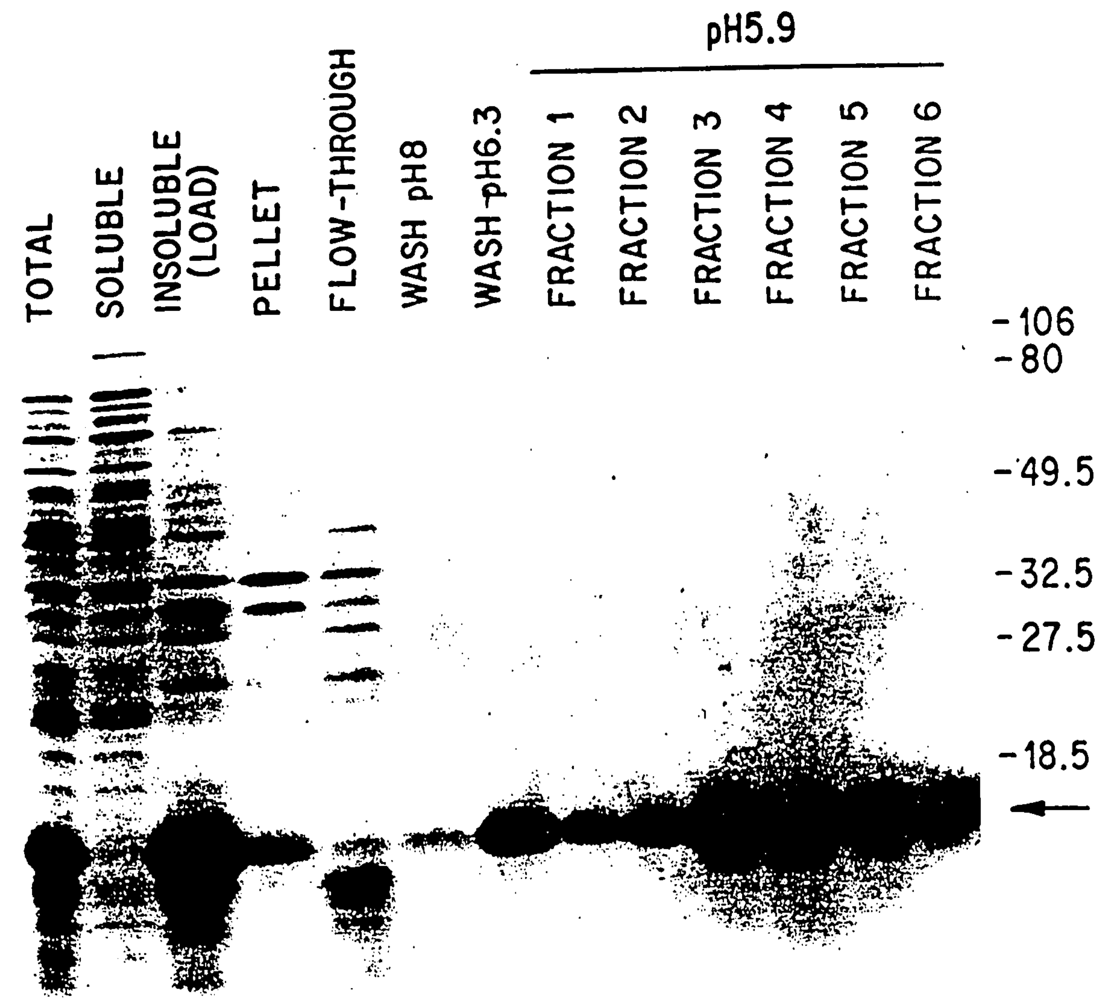

pH5.9
TOTAL
SOLUBLE
INSOLUBLE (LOAD)
PELLET
FLOW-THROUGH
WASH pH8
WASH-pH6.3
FRACTION 1
FRACTION 2
FRACTION 3
FRACTION 4
FRACTION 5
FRACTION 6
-106
-80
-49.5
-32.5
-27.5
-18.5

FIG. 8

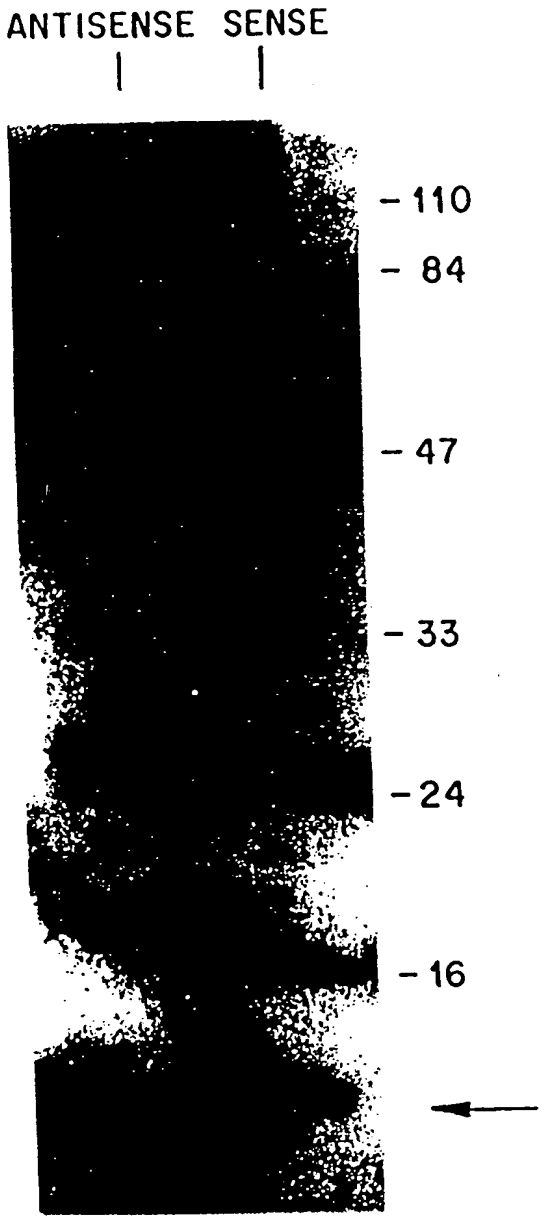


FIG. 9

FIG. 10A

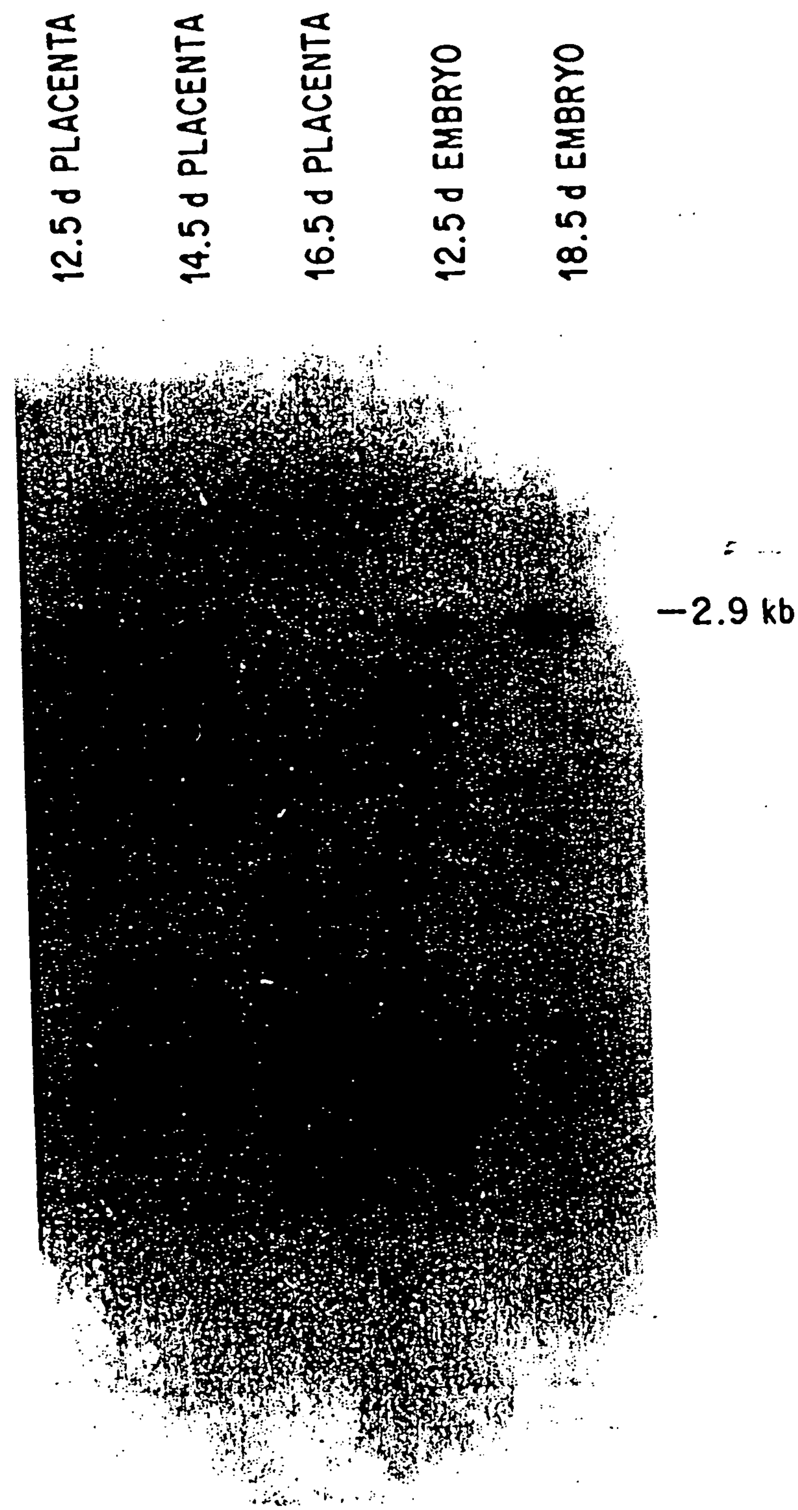

12.5 d PLACENTA
14.5 d PLACENTA
16.5 d PLACENTA
12.5 d EMBRYO
18.5 d EMBRYO
—2.9 kb

FIG. 10B

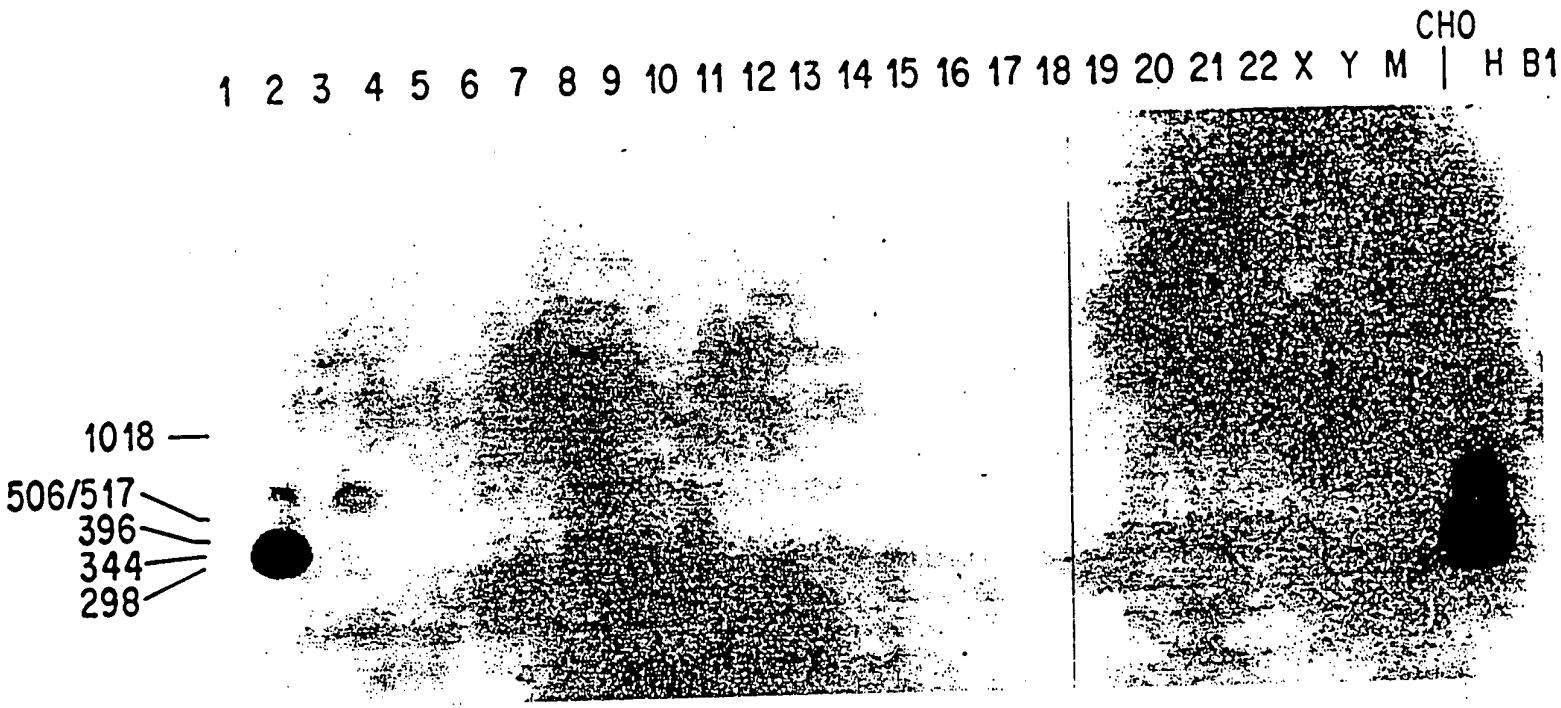

1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 X Y M
CHO
H B1
1018
506/517
396
344
298

FIG. 11

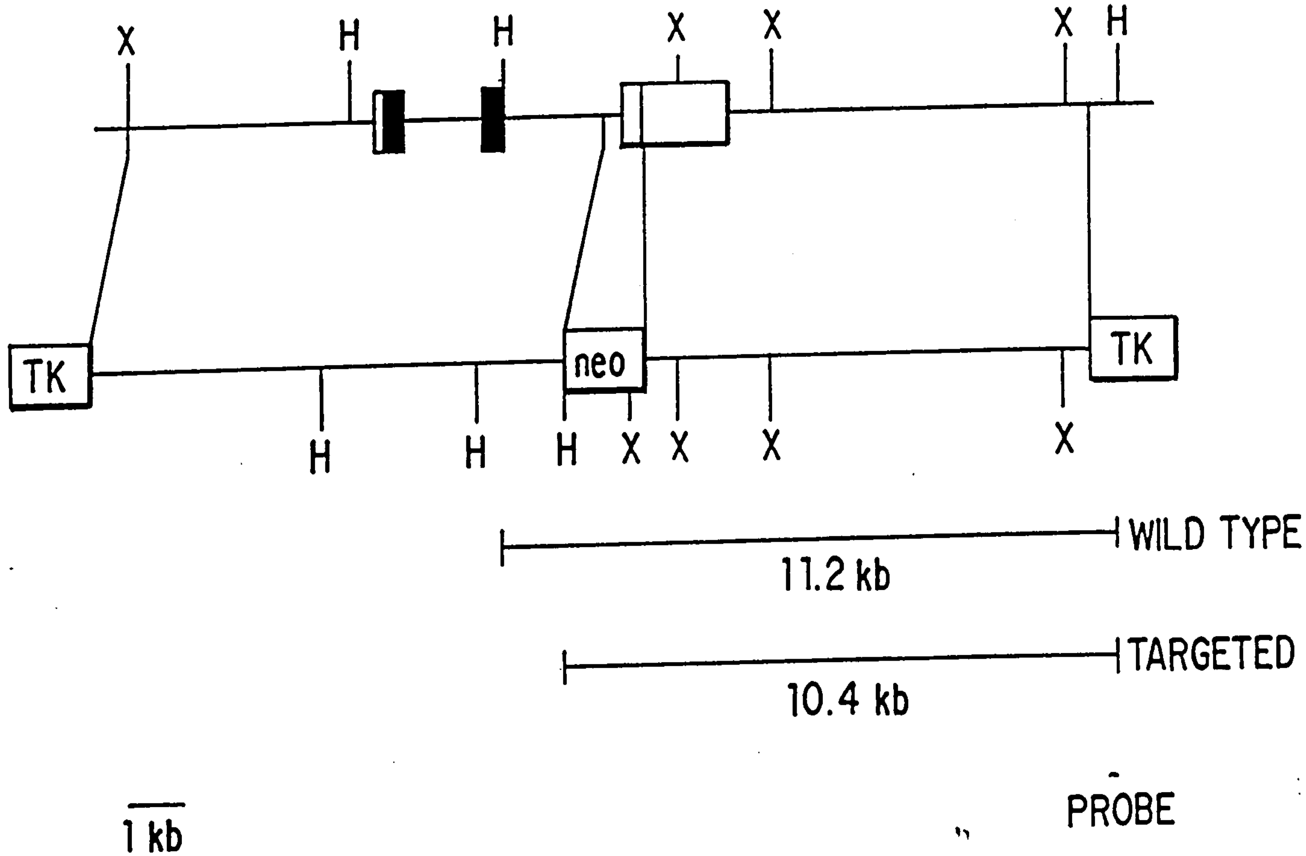


FIG. 12A

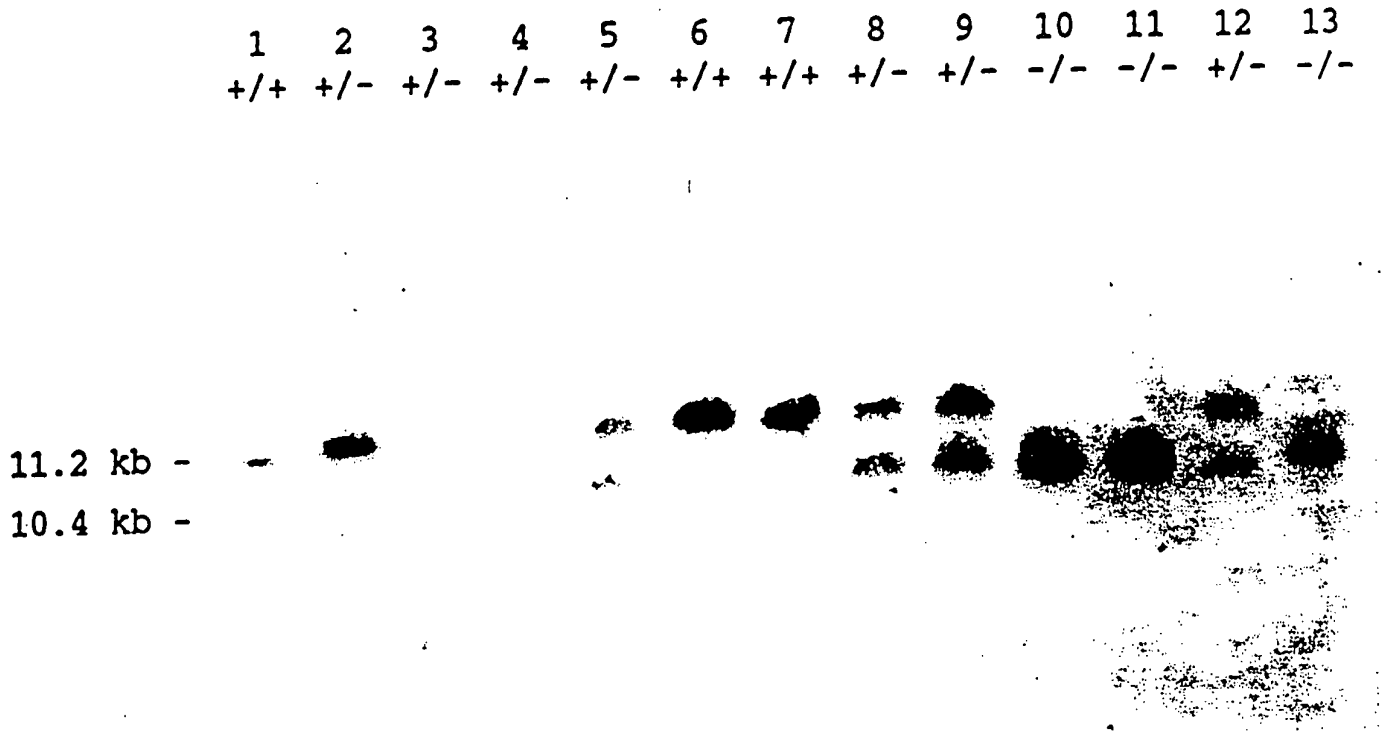


FIG. 12B

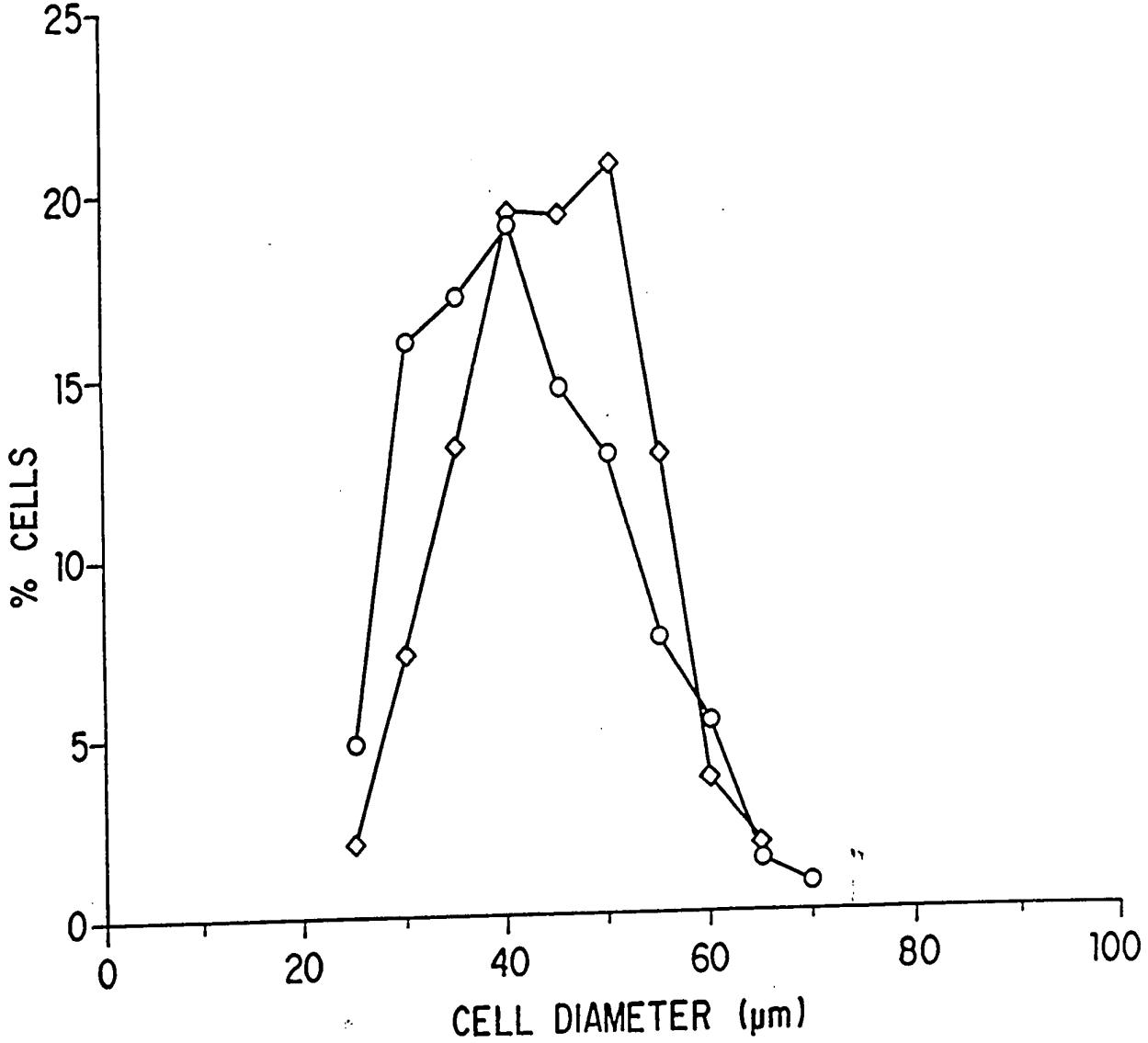


FIG. 13A

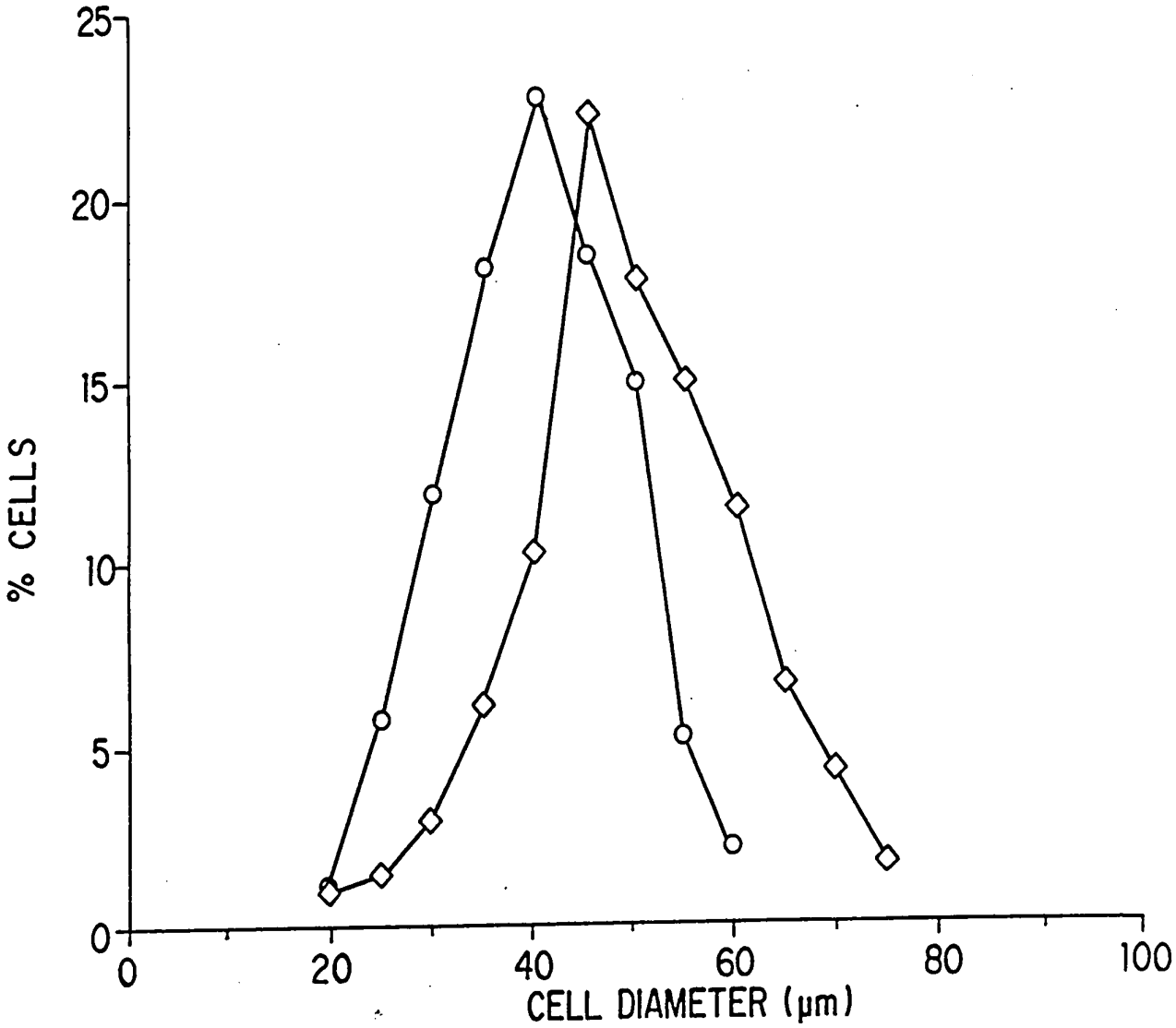


FIG. 13B

Cod DNA
[Strand]

```
1    ACTCCCCCGAGTCCCGGTGCTGCCGCTACCCCCTCACAGTGGACTTTGAAGACTTTGGCTGGGACTGGGTGATCGCGCCCAAGCG
       S  P  E  S  R  C  C  R  Y  P  L  T  V  D  F  E  D  F  G  W  D  W  V  I  A  P  K  R

86   ATACAAGGCCAACTATTGCTCCGGGGAGTGTGAGTACATGTACCTGCAGAAGTACCCCCACACCCACCTGGTGCACAAGGCCAGC
       Y  K  A  N  Y  C  S  G  E  C  E  Y  M  Y  L  Q  K  Y  P  H  T  H  L  V  H  K  A  S

171  CCCCGGGGCAACGCTGGGCCCTGCTGCACGCCCACCAAGATGTCCCCCATCAACATGCTCTACTTCAACCGCAAGGAGCAGATCA
       P  R  G  N  A  G  P  C  C  T  P  T  K  M  S  P  I  N  M  L  Y  F  N  R  K  E  Q  I

256  TCTACGGCAAGCTGCCCTCTATGGTCGTA
       I  Y  G  K  L  P  S  M  V  V
```

FIG. 14

Sea Bass
[Strand]

```
1    TGCTGCCGCTACCCACTCACAGTGGACTTTGAAGACTTTGGTTGGGACTGGATTATTGCCCCAAAGCGCTACAAGGCCAACTATT
       C  C  R  Y  P  L  T  V  D  F  E  D  F  G  W  D  W  I  I  A  P  K  R  Y  K  A  N  Y

86   GCTCCGGGGAGTGTGAGTACATGCACTTGCAGAAGTATCCGCACACCCACCTGGTGAACAAAGCCAACCCCAGAGGGACCGCGGG
       C  S  G  E  C  E  Y  M  H  L  Q  K  Y  P  H  T  H  L  V  N  K  A  N  P  R  G  T  A  G

171  TCCCTGCTGCACCCCGACCAAGATGTCGCCCATNAACATGCTCTACTTTAACCGAAAAGAGCAGATAATCTACGGCAAGATCCCT
       P  C  C  T  P  T  K  M  S  P  ?  N  M  L  Y  F  N  R  K  E  Q  I  I  Y  G  K  I  P

256  TCCATGGTGGTG
       S  M  V  V
```

FIG. 15

Sea Bream DNA
[Strand]

```
1    TCTCAGAGTCCCGGTGCTGCCGCTACCCGCTCACGGTGGACTTCGAAGACTTTGGCTGGGACTGGATTATTGCCCCAAAGCGCTA
       S  E  S  R  C  C  R  Y  P  L  T  V  D  F  E  D  F  G  W  D  W  I  I  A  P  K  R  Y

86   CAAGGCCAACTATTGCTCCGGGGAGTGTGAGTACATGCACTTGCAGAAGTACCCGCACACCCACCTGGTGAACAAAGCCAACCCC
       K  A  N  Y  C  S  G  E  C  E  Y  M  H  L  Q  K  Y  P  H  T  H  L  V  N  K  A  N  P

171  AGAGGGTCCGCGGGCCCCTGCTGTACCCCCACCAAGATGTCGCCCATCAACATGCTCTACTTTAACCGAAAGGAGCAGATCATCT
       R  G  S  A  G  P  C  C  T  P  T  K  M  S  P  I  N  M  L  Y  F  N  R  K  E  Q  I  I

256  ACGGCAAGATCCCGTCCATGGTGGTA
       Y  G  K  I  P  S  M  V  V
```

FIG. 16

Tautog DNA
[Strand]

```
1    CTCAGAGTCCCGGTGCTGCCGCTACCCACTCACAGTGGACTTTGAAGACTTTGGCTGGGACTGGATTATTGCTCCAAAGCGCTAC
       S  E  S  R  C  C  R  Y  P  L  T  V  D  F  E  D  F  G  W  D  W  I  I  A  P  K  R  Y

86   AAGGCCAACTATTGCTCCGGGGAGTGTGAGTACATGCACCTGCAGAAGTACCCGCACACCCACCTCGTGAACAAAGCCAACCCCA
       K  A  N  Y  C  S  G  E  C  E  Y  M  H  L  Q  K  Y  P  H  T  H  L  V  N  K  A  N  P

171  GAGGGACTGCAGGCCCCTGCTGCACCCCCACCAAGATGTCGCCCATCAACATGCTCTACTTTAACCGAAAGGAGCAGATCATCTA
       R  G  T  A  G  P  C  C  T  P  T  K  M  S  P  I  N  M  L  Y  F  N  R  K  E  Q  I  I  Y

256  CGGCAAGATCCCCTCCATGGTGGTG
       G  K  I  P  S  M  V  V
```

FIG. 17

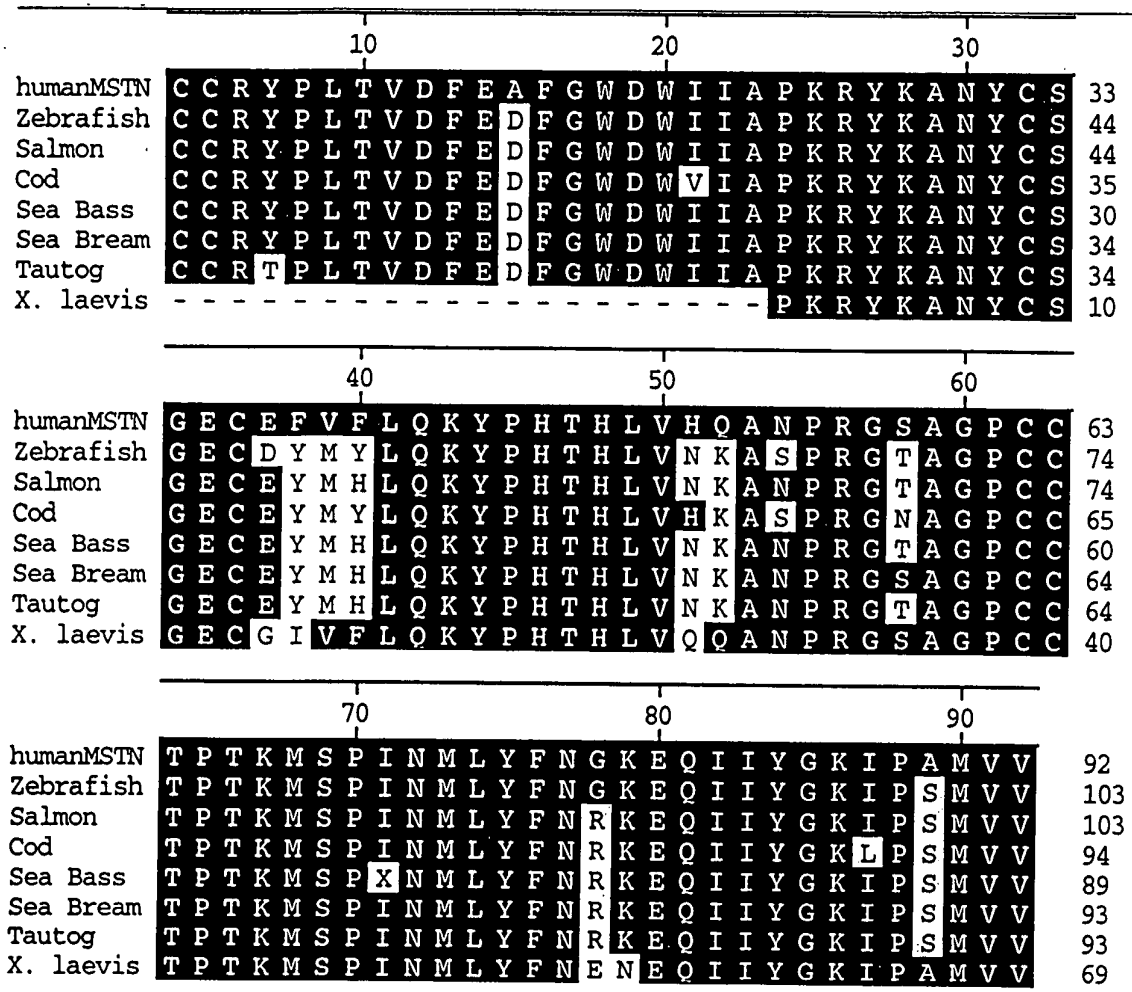
X. laevis T7
[Strand]

```
1    TCCAAAACGATATAAAGCCAACTATTGCTCTGGAGAGTGCGGCATTGTCTTTTTGCAAAAGTACCCGCACACACATCTTGTTCAA
       P  K  R  Y  K  A  N  Y  C  S  G  E  C  G  I  V  F  L  Q  K  Y  P  H  T  H  L  V  Q

86   CAAGCAAACCCCAGAGGTTCTGCTGGCCCTTGCTGTACCCCAACCAAAATGTCCCCAATTAATATGTTGTATTTCAATGAAAATG
       Q  A  N  P  R  G  S  A  G  P  C  C  T  P  T  K  M  S  P  I  N  M  L  Y  F  N  E  N

171  AACAAATCATATATGGAAAAATTCCAGCTATGGTGGTA
       E  Q  I  I  Y  G  K  I  P  A  M  V  V
```

FIG. 18



Decoration 'Decoration #1': Shade (with solid black) residues that match humanMSTN exactly.

FIG. 19

Percent Similarity

Percent Divergence

	1	2	3	4	5	6	7	8		
1		88.8	89.9	87.6	88.8	91.0	88.8	92.8	1	humanMSTN
2	11.2		95.5	93.3	94.4	94.4	94.4	84.1	2	Zebrafish
3	10.1	4.5		93.3	98.9	98.9	98.9	85.5	3	Salmon
4	12.4	6.7	6.7		92.1	93.3	92.1	82.6	4	Cod
5	10.2	4.5	0.0	6.8		97.8	97.8	84.1	5	Sea Bass
6	9.0	5.6	1.1	6.7	1.1		97.8	87.0	6	Sea Bream
7	11.2	5.6	1.1	7.9	1.1	2.2		85.5	7	Tautog
8	7.2	15.9	14.5	17.4	14.7	13.0	14.5		8	X. laevis
	1	2	3	4	5	6	7	8		

FIG. 20

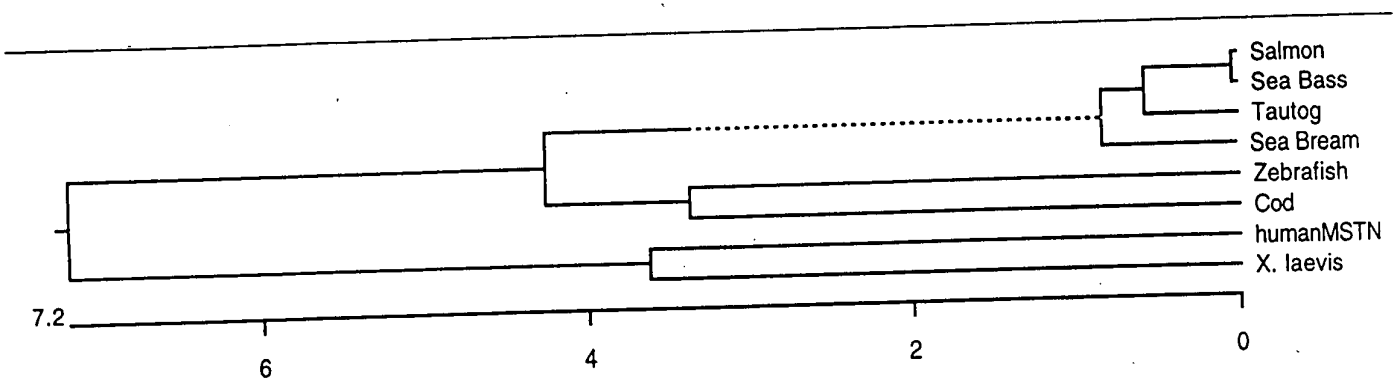

Salmon
Sea Bass
Tautog
Sea Bream
Zebrafish
Cod
humanMSTN
X. laevis
7.2
6
4
2
0

FIG. 21